



SUBSTITUTE SEQUENCE LISTING

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<120> EXTENDED CDNAS FOR SECRETED PROTEINS

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<140> 09/191,997

<141> 1998-11-13

<150> 60/066,677

<151> 1997-11-13

<150> 60/069,957

<151> 1997-12-17

<150> 60/074,121

<151> 1998-02-09

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 tttttvn 67

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aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca	60
gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc	113
Met Lys Lys Val Leu Leu Leu Ile	
-15 -10	
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag	161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln	
-5 1 5	
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr	209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly	
10 15 20	
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att	257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile	
25 30 35	
cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata	305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile	
40 45 50 55	
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa	354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys	
60 65	
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat	414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta	474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa	526

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<221> SIGNAL
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      seq LLLITAILAVAVG/FP
<400> 18
Met Lys Lys Val Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1          5          10          15
Gly

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<210> 19
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<222> 56..113
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<222> 118..545
<223> blastn
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<221> misc_feature
<222> 65..369
<223> blastn
<220>
<221> misc_feature
<222> 61..399
<223> blastn
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<222> 408..458
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<222> 346..408
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actccttttta gcataggggc ttcggcgccca gcggccagcg ctagtcgggc tggtaagtgc      60
ctgatgccga gttccgtctc tcgcgtcttt tcttggtccc aggcaaagcg gasgnagatc      120
ctcaaacggc ctagtgcttc gcgcttcggg agaaaatcag cggctctaatt aattcctctg      180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca      240
cgttcctggt gagtacacgt tctgttgat ttacaaaagg tgcaggatg agcaggctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                     Met Trp Trp Phe
                                     -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                      5                      10                      15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
      20                      25                      30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                      40                      45
aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgacccaaa      602
Lys
ctcttcaraa acatgtcttt acaagcatat ctcttgatt gctttctaca ctgttgaatt      662
gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg      722
gtaagggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw      782
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa      822

<210> 20
<211> 21
<212> PRT
<213> Homo Sapiens
<220>
<221> SIGNAL
<222> 1..21
<223> Von Heijne matrix
      score 5.5
      seq SFLPSALVIWTS/AF
<400> 20
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
1                      5                      10                      15
Ile Trp Thr Ser Ala
      20

<210> 21
<211> 405
<212> DNA
<213> Homo Sapiens
<220>

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<222> complement(103..398)
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<221> sig_peptide
<222> 185..295
<223> Von Heijne matrix
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atcaccttct tctccatcct tstctgggcc agtccccarc ccagtccttc tctgacctg      60
cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct      120
ggcattccag gacctccgma atgatgctcc agtcctttac aagcgcttcc tggatgaggg      180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg      229
      Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
            -35                    -30                    -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
            -20                    -15                    -10
ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
            -5                    1                    5                    10
cct gac aac taaatatcct tatccaaatc aataaarwra raatcctccc      374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaaa a      405

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<213> Homo Sapiens
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<221> SIGNAL
<222> 1..37
<223> Von Heijne matrix
      score 5.9
      seq LSYASSALSPCLT/AP
<400> 22
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1                    5                    10                    15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
      20                    25                    30
Ser Pro Cys Leu Thr
      35

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attagccgtg gcctaggccg tttaacgggg tgacacgagc ntgcagggcc gagtccaagg      120
cccgagata ggaccaaccg tcaggaatgc gaggaatggt tttcttcgga ctctatcgag      180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt      231
                Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
                -15                -10                -5

gcc ara gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt      279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
                1                5                10
gag aag cac aga ctc gag aaa tgt agg gaa ctc gag asc asc cac tcg      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
                15                20                25
gcc cca gga tca acc cas cac cga aga aaa aca acc aga aga aat tat      375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
                30                35                40                45
tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc      424
Ser Ser Ala
atattttaat tggaaaagtc aaattgasca ttattaaata aagcttggtt aatatgtctc      484
aaacaaaaaa aa      496

<210> 24
<211> 15
<212> PRT
<213> Homo Sapiens
<220>
<221> SIGNAL
<222> 1..15
<223> Von Heijne matrix
        score 5.5
        seq ILSTVTALTFAXA/LD
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<221> UNSURE
<222> 14
<223> Xaa = any one of the twenty amino acids
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Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
1                5                10                15

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<211> 623
<212> DNA
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<223> Von Heijne matrix
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aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg      57
                Met Glu Arg

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                                     -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10      -5      1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5      10      15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20      25      30      35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
      40      45      50
cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac      297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
      55      60      65
atg aak ttc gaa tgg tgc ccg gcc ccc atg gtg caa ggc gtg atc acc      345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
      70      75      80
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag      393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
      85      90      95
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg      441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100      105      110      115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
      120      125      130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
      135      140      145
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa      594
taaactctca tgcccccaaa aaaaaaaaaa      623

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<210> 26
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<212> PRT
<213> Homo Sapiens
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<222> 1..16
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1      5      10      15

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<210> 27
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<222> 32..73
<223> Von Heijne matrix
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Met Leu Trp Leu Leu Phe Phe

-10

ctg	gtg	act	gcc	att	cat	gct	gaa	ctc	tgt	caa	cca	ggt	gca	gaa	aat	100
Leu	Val	Thr	Ala	Ile	His	Ala	Glu	Leu	Cys	Gln	Pro	Gly	Ala	Glu	Asn	
		-5				1				5						
gct	ttt	aaa	gtg	aga	ctt	agt	atc	aga	aca	gct	ctg	gga	gat	aaa	gca	148
Ala	Phe	Lys	Val	Arg	Leu	Ser	Ile	Arg	Thr	Ala	Leu	Gly	Asp	Lys	Ala	
10				15					20					25		
tat	gcc	tgg	gat	acc	aat	gaa	gaa	tac	ctc	ttc	aaa	gcg	atg	gta	gct	196
Tyr	Ala	Trp	Asp	Thr	Asn	Glu	Glu	Tyr	Leu	Phe	Lys	Ala	Met	Val	Ala	
			30					35					40			
ttc	tcc	atg	aga	aaa	gtt	ccc	aac	aga	gaa	gca	aca	gaa	att	tcc	cat	244
Phe	Ser	Met	Arg	Lys	Val	Pro	Asn	Arg	Glu	Ala	Thr	Glu	Ile	Ser	His	
			45				50					55				
gtc	cta	ctt	tgc	aat	gta	acc	cag	agg	gta	tca	ttc	tgg	ttt	gtg	gtt	292
Val	Leu	Leu	Cys	Asn	Val	Thr	Gln	Arg	Val	Ser	Phe	Trp	Phe	Val	Val	
		60				65				70						
aca	gac	cct	tca	aaa	aat	cac	acc	ctt	cct	gct	ggt	gag	gtg	caa	tca	340
Thr	Asp	Pro	Ser	Lys	Asn	His	Thr	Leu	Pro	Ala	Val	Glu	Val	Gln	Ser	
	75				80					85						
gcc	ata	aga	atg	aac	aag	aac	cgg	atc	aac	aat	gcc	ttc	ttt	cta	aat	388
Ala	Ile	Arg	Met	Asn	Lys	Asn	Arg	Ile	Asn	Asn	Ala	Phe	Phe	Leu	Asn	
90				95					100					105		
gac	caa	act	ctg	gaa	ttt	tta	aaa	atc	cct	tcc	aca	ctt	gca	cca	ccc	436
Asp	Gln	Thr	Leu	Glu	Phe	Leu	Lys	Ile	Pro	Ser	Thr	Leu	Ala	Pro	Pro	
			110					115					120			
atg	gac	cca	tct	gtg	ccc	atc	tgg	att	att	ata	ttt	ggt	gtg	ata	ttt	484
Met	Asp	Pro	Ser	Val	Pro	Ile	Trp	Ile	Ile	Ile	Phe	Gly	Val	Ile	Phe	
		125				130						135				
tgc	atc	atc	ata	gtt	gca	att	gca	cta	ctg	att	tta	tca	ggg	atc	tgg	532
Cys	Ile	Ile	Val	Ala	Ile	Ala	Leu	Leu	Ile	Leu	Ser	Gly	Ile	Trp		
	140				145					150						
caa	cgt	ada	ara	aag	aac	aaa	gaa	cca	tct	gaa	gtg	gat	gac	gct	gaa	580
Gln	Arg	Xaa	Xaa	Lys	Asn	Lys	Glu	Pro	Ser	Glu	Val	Asp	Asp	Ala	Glu	
	155			160						165						
rat	aak	tgt	gaa	aac	atg	atc	aca	att	gaa	aat	ggc	atc	ccc	tct	gat	628
Xaa	Xaa	Cys	Glu	Asn	Met	Ile	Thr	Ile	Glu	Asn	Gly	Ile	Pro	Ser	Asp	
170				175					180					185		
ccc	ctg	gac	atg	aag	gga	ggg	cat	att	aat	gat	gcc	ttc	atg	aca	gag	676
Pro	Leu	Asp	Met	Lys	Gly	Gly	His	Ile	Asn	Asp	Ala	Phe	Met	Thr	Glu	
			190					195				200				
gat	gag	agg	ctc	acc	cct	ctc	tga	agg	gctg	ttgttctgct	tcctcaaraa					727
Asp	Glu	Arg	Leu	Thr	Pro	Leu										
			205													
attaaacatt	tgtttctgtg	tgactgctga	gcacccctgaa	ataccaagag	cagatcatat											787
wttttgtttc	accattcttc	ttttgtaata	aattttgaat	gtgcttgaaa	aaaaaaaaaa											847
c																848

<210> 28

<211> 14

<212> PRT

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<220>

<221> SIGNAL

<222> 1..14

<223> Von Heijne matrix

score 10.7

seq LWLLFFLVTAIHA/EL

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Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala  
1 5 10

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<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

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gggaagatgg agatagtatt gcctg

25

<210> 30

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 30

ctgccatgta catgatagag agattc

26

<210> 31

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<222> 1..517

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<222> 518

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<221> protein\_bind

<222> 17..25

<223> matinspector prediction

name CMYB\_01

score 0.983

sequence tgtcagttg

<220>

<221> protein\_bind

<222> complement(18..27)

<223> matinspector prediction

name MYOD\_Q6

score 0.961

sequence cccaactgac

<220>

<221> protein\_bind

<222> complement(75..85)

<223> matinspector prediction

name S8\_01

score 0.960

sequence aatagaattag

<220>

<221> protein\_bind

<222> 94..104

<223> matinspector prediction

name S8\_01

score 0.966  
 sequence aactaaattag  
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 <222> complement(129..139)  
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     name DELTAEF1\_01  
     score 0.960  
     sequence gcacacctcag  
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 <222> complement(155..165)  
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     name GATA\_C  
     score 0.964  
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     name CMYB\_01  
     score 0.958  
     sequence cttcagttg  
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     name GATA1\_02  
     score 0.959  
     sequence ttgtagataggaca  
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 <222> 180..190  
 <223> matinspector prediction  
     name GATA\_C  
     score 0.953  
     sequence agataggacat  
 <220>  
 <221> protein\_bind  
 <222> 284..299  
 <223> matinspector prediction  
     name TAL1ALPHA47\_01  
     score 0.973  
     sequence cataacagatggtaag  
 <220>  
 <221> protein\_bind  
 <222> 284..299  
 <223> matinspector prediction  
     name TAL1BETA47\_01  
     score 0.983  
     sequence cataacagatggtaag  
 <220>  
 <221> protein\_bind  
 <222> 284..299  
 <223> matinspector prediction  
     name TAL1BETAITF2\_01  
     score 0.978  
     sequence cataacagatggtaag

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<220>
<221> protein_bind
<222> complement(287..296)
<223> matinspector prediction
      name MYOD_Q6
      score 0.954
      sequence accatctggt
<220>
<221> protein_bind
<222> complement(302..314)
<223> matinspector prediction
      name GATA1_04
      score 0.953
      sequence tcaagataaagta
<220>
<221> protein_bind
<222> 393..405
<223> matinspector prediction
      name IK1_01
      score 0.963
      sequence agttgggaattcc
<220>
<221> protein_bind
<222> 393..404
<223> matinspector prediction
      name IK2_01
      score 0.985
      sequence agttgggaattc
<220>
<221> protein_bind
<222> 396..405
<223> matinspector prediction
      name CREL_01
      score 0.962
      sequence tgggaattcc
<220>
<221> protein_bind
<222> 423..436
<223> matinspector prediction
      name GATA1_02
      score 0.950
      sequence tcagtgatatggca
<220>
<221> protein_bind
<222> complement(478..489)
<223> matinspector prediction
      name SRY_02
      score 0.951
      sequence taaaacaaaaca
<220>
<221> protein_bind
<222> 486..493
<223> matinspector prediction
      name E2F_02
      score 0.957
      sequence tttagcgc
<220>
<221> protein_bind

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```

<222> complement(514..521)
<223> matinspector prediction
      name MZF1_01
      score 0.975
      sequence tgagggga
<400> 31
tgagtgcagt gttacatgtc agttgggtta agtttggtta tgtcattcaa atcttctatg      60
tcttgatttg cctgctaatt ctattatttc tggaactaaa ttagtttgat ggttctatta      120
gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta      180
gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa      240
atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg      300
atactttatc ttgagtagga gaggcttcct gtggcaacgt ggagaaggga agaggtcgta      360
gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag      420
catcagtgat atggcaaagt tgggactaag ggtagtgatc agaggggttaa aattgtgtgt      480
tttgttttag cgctgctggg gcatcgctt gggtcccctc aaacagattc ccatgaatct      540
cttcat      546

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide
<400> 32
gtaccaggga ctgtgaccat tgc      23

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide
<400> 33
ctgtgaccat tgctcccaag agag      24

<210> 34
<211> 861
<212> DNA
<213> Homo Sapiens
<220>
<221> promoter
<222> 1..806
<220>
<221> transcription start site
<222> 807
<220>
<221> protein_bind
<222> complement(60..70)
<223> matinspector prediction
      name NFY_Q6
      score 0.956
      sequence ggaccaatcat
<220>
<221> protein_bind
<222> 70..77
<223> matinspector prediction
      name MZF1_01
      score 0.962

```

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sequence cctgggga
<220>
<221> protein_bind
<222> 124..132
<223> matinspector prediction
      name CMYB_01
      score 0.994
      sequence tgaccgttg
<220>
<221> protein_bind
<222> complement(126..134)
<223> matinspector prediction
      name VMYB_02
      score 0.985
      sequence tccaacggt
<220>
<221> protein_bind
<222> 135..143
<223> matinspector prediction
      name STAT_01
      score 0.968
      sequence ttcctggaa
<220>
<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
      name STAT_01
      score 0.951
      sequence ttccaggaa
<220>
<221> protein_bind
<222> complement(252..259)
<223> matinspector prediction
      name MZF1_01
      score 0.956
      sequence ttggggga
<220>
<221> protein_bind
<222> 357..368
<223> matinspector prediction
      name IK2_01
      score 0.965
      sequence gaatgggatttc
<220>
<221> protein_bind
<222> 384..391
<223> matinspector prediction
      name MZF1_01
      score 0.986
      sequence agagggga
<220>
<221> protein_bind
<222> complement(410..421)
<223> matinspector prediction
      name SRY_02
      score 0.955
      sequence gaaaacaaaaca
<220>

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<221> protein\_bind  
 <222> 592..599  
 <223> matinspector prediction  
       name MZF1\_01  
       score 0.960  
       sequence gaagggga

<220>  
 <221> protein\_bind  
 <222> 618..627  
 <223> matinspector prediction  
       name MYOD\_Q6  
       score 0.981  
       sequence agcatctgcc

<220>  
 <221> protein\_bind  
 <222> 632..642  
 <223> matinspector prediction  
       name DELTAEF1\_01  
       score 0.958  
       sequence tcccaccttc

<220>  
 <221> protein\_bind  
 <222> complement(813..823)  
 <223> matinspector prediction  
       name S8\_01  
       score 0.992  
       sequence gaggcaattat

<220>  
 <221> protein\_bind  
 <222> complement(824..831)  
 <223> matinspector prediction  
       name MZF1\_01  
       score 0.986  
       sequence agagggga

<220>  
 <221> misc\_feature  
 <222> 335,376  
 <223> n=a, g, c or t  
 <400> 34

tactataggg	cacgcgtggt	cgacggccgg	gctgttctgg	agcagagggc	atgtcagtaa	60
tgattggtcc	ctggggaagg	tctggctggc	tccagcacag	tgaggcattt	aggtatctct	120
cggtgaccgt	tggattcctg	gaagcagtag	ctgttctggt	tggatctggt	agggacaggg	180
ctcagagggc	taggcacgag	ggaaggtcag	aggagaaggs	aggsarggcc	cagtgagarg	240
ggagcatgcc	ttcccccaac	cctggcttsc	ycttggyam	agggcgkty	tgggmacttr	300
aaytcagggc	ccaascagaa	scacaggccc	aktcntggct	smaagcacia	tagcctgaat	360
gggatttcag	gttagncagg	gtgagagggg	aggctctctg	gcttagtttt	gttttgtttt	420
ccaaatcaag	gtaacttgct	cccttctgct	acgggccttg	gtcttggttt	gtcctcaccc	480
agtcggaact	ccctaccact	ttcaggagag	tggttttagg	cccgtggggc	tgttctgttc	540
caagcagtg	gagaacatgg	ctggtagagg	ctctagctgt	gtgcggggcc	tgaaggggag	600
tgggttctcg	cccaaagagc	atctgccc	ttcccacctt	cccttctccc	accagaagct	660
tgcttgagct	gttttgacaa	aaatccaaac	cccacttggc	tactctggcc	tggcttcagc	720
ttggaacca	atacctaggc	ttacaggcca	tcctgagcca	ggggcctctg	gaaattctct	780
tcctgatggt	cctttaggtt	tgggcacaaa	atataattgc	ctctcccctc	tcccattttc	840
tctcttggga	gcaatggtca	c				861

<210> 35  
 <211> 20  
 <212> DNA



<213> Artificial Sequence  
 <220>  
 <223> oligonucleotide  
 <400> 35  
 ctgggatgga aggcacggtg

20

<210> 36  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> oligonucleotide  
 <400> 36  
 gagaccacac agctagacaa

20

<210> 37  
 <211> 555  
 <212> DNA  
 <213> Homo Sapiens  
 <220>  
 <221> promoter  
 <222> 1..500  
 <220>  
 <221> transcription start site  
 <222> 501  
 <220>  
 <221> protein\_bind  
 <222> 191..206  
 <223> matinspector prediction  
     name ARNT\_01  
     score 0.964  
     sequence ggactcacgtgctgct  
 <220>  
 <221> protein\_bind  
 <222> 193..204  
 <223> matinspector prediction  
     name NMYC\_01  
     score 0.965  
     sequence actcacgtgctg  
 <220>  
 <221> protein\_bind  
 <222> 193..204  
 <223> matinspector prediction  
     name USF\_01  
     score 0.985  
     sequence actcacgtgctg  
 <220>  
 <221> protein\_bind  
 <222> complement(193..204)  
 <223> matinspector prediction  
     name USF\_01  
     score 0.985  
     sequence cagcacgtgagt  
 <220>  
 <221> protein\_bind  
 <222> complement(193..204)  
 <223> matinspector prediction  
     name NMYC\_01

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        score 0.956
        sequence cagcacgtgagt
<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
        name MYCMAX_02
        score 0.972
        sequence cagcacgtgagt
<220>
<221> protein_bind
<222> 195..202
<223> matinspector prediction
        name USF_C
        score 0.997
        sequence tcacgtgc
<220>
<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
        name USF_C
        score 0.991
        sequence gcacgtga
<220>
<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
        name MZF1_01
        score 0.968
        sequence catgggga
<220>
<221> protein_bind
<222> 397..410
<223> matinspector prediction
        name ELK1_02
        score 0.963
        sequence ctctccggaagcct
<220>
<221> protein_bind
<222> 400..409
<223> matinspector prediction
        name CETS1P54_01
        score 0.974
        sequence tccggaagcc
<220>
<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
        name AP1_Q4
        score 0.963
        sequence agtgactgaac
<220>
<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
        name AP1FJ_Q2
        score 0.961
        sequence agtgactgaac

```

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<220>
<221> protein_bind
<222> 547..555
<223> matinspector prediction
      name PADS_C
      score 1.000
      sequence tgttgtctc
<400> 37
ctatagggca cgcktggtcg acggcccggt ctggtctggt ctgtkgtgga gtcgggttga      60
aggacagcat ttgtkacatc tgggtctactg caccttccct ctgccgtgca cttggccttt      120
kawaagctca gcaccggtgc ccatcacagg gccggcagca cacacatccc attactcaga      180
aggaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta      240
gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaatcc aagtgattgt      300
cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag      360
gttgctctgc ccattggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc      420
cgtgtcttct gcctgtctcc gctcacatcc cacacttggt ttcagtcact gagttacaga      480
ttttgcctcc tcaatttctc ttgtcttagt cccatcctct gttcccctgg ccagtttgtc      540
tagctgtgtg gtctc                                     555

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide
<400> 38
ggccatacac ttgagtgac                                     19

<210> 39
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide
<400> 39
atatagacaa acgcacacc                                     19

<210> 40
<211> 1098
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 173..211
<223> Von Heijne matrix
      score 4.19999980926514
      seq MLAVSLTVPLLGA/MM
<220>
<221> polyA_signal
<222> 1063..1068
<220>
<221> polyA_site
<222> 1087..1098
<220>
<221> misc_feature
<222> 144..467
<223> homology
      id :AA057573

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    est
<220>
<221> misc_feature
<222> 510..640
<223> homology
    id :AA057573
    est
<220>
<221> misc_feature
<222> 436..523
<223> homology
    id :AA057573
    est
<220>
<221> misc_feature
<222> 708..786
<223> homology
    id :AA057573
    est
<220>
<221> misc_feature
<222> 635..682
<223> homology
    id :AA057573
    est
<220>
<221> misc_feature
<222> 625..1084
<223> homology
    id :N57409
    est
<220>
<221> misc_feature
<222> 779..1084
<223> homology
    id :R71351
    est
<220>
<221> misc_feature
<222> 144..506
<223> homology
    id :H12619
    est
<220>
<221> misc_feature
<222> 90..467
<223> homology
    id :T03538
    est
<220>
<221> misc_feature
<222> 314..523
<223> homology
    id :T34150
    est
<220>
<221> misc_feature
<222> 567..687

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<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 686..730
<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 510..553
<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 550..579
<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 144..523
<223> homology
      id :N32314
      est
<220>
<221> misc_feature
<222> 510..553
<223> homology
      id :N32314
      est
<220>
<221> misc_feature
<222> 352..523
<223> homology
      id :T77966
      est
<220>
<221> misc_feature
<222> 218..351
<223> homology
      id :T77966
      est
<220>
<221> misc_feature
<222> 510..553
<223> homology
      id :T77966
      est
<220>
<221> misc_feature
<222> 550..917
<223> homology
      id :AA464128
      est
<220>

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<221> misc_feature
<222> 1083
<223> n=a, g, c or t
<400> 40
agtgaggtgg tttctgcggg tgaggctggc gcccgtacca tgagcggaggc ggacgggctg      60
cgacagcgcc ggcccctgcg gcccgcgaagt cgtcacagac gatgatggcc agggccccgga      120
ggctaaggac ggcagctcct ttagcggcag agttttccga gtgaccttct tg atg ctg      178
                                         Met Leu
gct gtt tct ctc acc gtt ccc ctg ctt gga gcc atg atg ctg ctg gaa      226
Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu Leu Glu
   -10                               -5                               1                               5
tct cct ata gat cca cag cct ctc agc ttc aaa gaa ccc ccg ctc ttg      274
Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu
               10                               15                               20
ctt ggt gtt ctg cat cca aat acg aag ctg cga cag gca gaa agg ctg      322
Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu
               25                               30                               35
ttt gaa aat caa ctt gtt gga ccg gag tcc ata gca cat att ggg gat      370
Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp
               40                               45                               50
gtg atg ttt act ggg aca gca gat ggc cgg gtc gta aaa ctt gaa aat      418
Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu Glu Asn
               55                               60                               65
ggg gaa ata gag acc att gcc cgg ttt ggt tcg ggc cct tgc aaa acc      466
Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys Lys Thr
               70                               75                               80                               85
cga ggt gat gag cct gtg tgt ggg aga ccc ctg ggt atc cgt ggc agg      514
Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg Gly Arg
               90                               95                               100
gcc caa tgg gac tct ctt tgt ggc cga tgc ata caa agg gac tat ttg      562
Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp Tyr Leu
               105                               110                               115
aag taaatccctg gaaacgtgaa gtgaaactgc tgctgtcctc cgagacaccc      615
Lys
attgaggggga agaacatgtc ctttgtgaat gatcttacag tcactcagga tgggaggaag      675
atattatttca ccgattctag cagcaaatgg caaagacgag actacctgct tctggtgatg      735
gagggcacag atgacgggcg cctgctggag tatgatactg tgaccagggga agtaaaagtt      795
ttattggacc agctgcggtt cccgaatgga gtccagctgt ctctgcaga agactttgtc      855
ctggtggcag aaacaacccat ggccaggata cgaagagtct acgtttctgg cctgatgaag      915
ggcgggggctg atctgtttgt ggagaacatg cctggatttc cagacaacat ccggcccagc      975
agctctggggg ggtactgggt gggcatgtcg accatccgcc ctaaccctgg gttttccatg     1035
ctggatttct tatctgagag accctggatt aaaaggatga tttttaangg taaaaaaaaa     1095
aaa                                                                1098

<210> 41
<211> 855
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 267..371
<223> Von Heijne matrix
      score 5.90000009536743
      seq LCGLLHLWLKVFS/LK
<220>
<221> polyA_signal
<222> 817..822
<220>

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<221> polyA_site
<222> 842..855
<220>
<221> misc_feature
<222> 608..811
<223> homology
      id :M85769
      est
<400> 41
acaatcagtt tgccaatacc tcagaaacaa atacctcgga caaatctttc tctaaagacc      60
tcagtcagat actagtcaat atcaaatacat gtagatggcg gcatttttagg cctcggacac      120
catccctaca tgacagtgcac aatgatgaac tctcctgtag aaaattatat aggagtataa      180
accgaacagg aacagcacaa cctgggaccc agacatgcag tacctctacg caaagtaaaa      240
gtagcagtggt ttcagcacac tttggt atg ttg act gtt aat gat gta cgt ttc      293
                               Met Leu Thr Val Asn Asp Val Arg Phe
                               -35                               -30
tat aga aat gtc agg tcc aac cat ttc cca ttt gtt cga cta tgt ggt      341
Tyr Arg Asn Val Arg Ser Asn His Phe Pro Phe Val Arg Leu Cys Gly
      -25                               -20                               -15
ctg tta cat tta tgg ctt aaa gtc ttt tct ctt aaa cag tta aaa aaa      389
Leu Leu His Leu Trp Leu Lys Val Phe Ser Leu Lys Gln Leu Lys Lys
      -10                               -5                               1                               5
aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg      437
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
      10                               15                               20
tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatggtttat      485
Tyr Val Cys Val Phe Ile
      25
ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca      545
tattttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga      605
tattttctcta gttttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg      665
cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt      725
cagagaagaa catttaaagg gttaatatatt ttgaaacggt ttcagataat atctatttga      785
ttattgtggc ttctatttga aatgtgtcta aaataaaatg ctgtttattt aaaatgaaaa      845
aaaaaaaaaa      855

<210> 42
<211> 1176
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 174..266
<223> Von Heijne matrix
      score 3.5
      seq WSPLSTRSGGTHA/CS
<220>
<221> polyA_signal
<222> 1144..1149
<220>
<221> polyA_site
<222> 1165..1176
<220>
<221> misc_feature
<222> 886..1134
<223> homology
      id :AA595193
      est

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<220>
<221> misc_feature
<222> 756..894
<223> homology
      id :AA595193
      est

<220>
<221> misc_feature
<222> 655..755
<223> homology
      id :AA595193
      est

<220>
<221> misc_feature
<222> 167..367
<223> homology
      id :W81213
      est

<220>
<221> misc_feature
<222> 66..172
<223> homology
      id :W81213
      est

<220>
<221> misc_feature
<222> 429..508
<223> homology
      id :W81213
      est

<220>
<221> misc_feature
<222> 756..894
<223> homology
      id :AA150887
      est

<220>
<221> misc_feature
<222> 536..643
<223> homology
      id :AA150887
      est

<220>
<221> misc_feature
<222> 655..755
<223> homology
      id :AA150887
      est

<220>
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<222> 429..643
<223> homology
      id :AA493644
      est

<220>
<221> misc_feature
<222> 655..755
<223> homology

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        id :AA493644
    est
<220>
<221> misc_feature
<222> 429..643
<223> homology
        id :AA493494
    est
<220>
<221> misc_feature
<222> 655..755
<223> homology
        id :AA493494
    est
<220>
<221> misc_feature
<222> 500..643
<223> homology
        id :AA179182
    est
<220>
<221> misc_feature
<222> 655..755
<223> homology
        id :AA179182
    est
<220>
<221> misc_feature
<222> 756..847
<223> homology
        id :AA179182
    est
<220>
<221> misc_feature
<222> 3..338
<223> homology
        id :HUM524F05B
    est
<220>
<221> misc_feature
<222> 334..374
<223> homology
        id :HUM524F05B
    est
<220>
<221> misc_feature
<222> 886..1134
<223> homology
        id :AA398156
    est
<220>
<221> misc_feature
<222> 756..894
<223> homology
        id :AA398156
    est
<220>
<221> misc_feature

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<222> 590,601

<223> n=a, g, c or t

<400> 42

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aaaaacaata ggacggaaac gccgaggaac ccggctgagg cggcagagca tcctggccag      60
aacaagccaa ggagccaaga cgagagggac acacggacaa acaacagaca gaagacgtac      120
tggccgctgg actccgctgc ctcccccatc tccccgccat ctgcgcccgagg agg atg      176
                                         Met
agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc tcc      224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30                               -25                -20                -15
ttc tgg agc cct ttg tcc acc agg tgc ggg ggc act cat gcg tgc tcc      272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
                               -10                -5                        1
gct tca atg aga caa ccc tgg gca agc ccc tgg tcc caa ggg aac atc      320
Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn Ile
                    5                10                15
agt tct acg aga ccc tcc ctg ctg aga tgc gca aat tct ctc ccc agt      368
Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro Ser
                20                25                30
aca aag gac aaa gcc aaa ggc ccc ttg tta gct ggc cat ccc tgc ccc      416
Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys Pro
35                               40                45                        50
att ttt tcc cct ggt cct ttc ccc tgt ggc cac agg gaa gtg tgg cct      464
Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp Pro
                    55                60                65
gaa tac ccc acc ccg gct cct ctg cac cca gag ctg ggg gcc acc tca      512
Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr Ser
                70                75                80
gaa gtg tca tct ctc tct gag cac gsa ttc ccc tgc agc agt cga gga      560
Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg Gly
                85                90                95
ctg agc aga ttg agt gat gct ggg gca gan adg cct gag ang aaa ggt      608
Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys Gly
100                105                110
gtt cag cca gtc gtt tgt aag gcg ctc gkc ggm act gct gaa acg ccc      656
Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr Pro
115                120                125                130
cca ccc tgacagcccc atcctcaaag actgtcttaa ttactcatgg caggttctag      712
Pro Pro
agacttaagg ggaaaagctg ctttcaaggc caccacatgt ctggtgctcc ccmaccagst      772
statctgcct wgtgttcatt ttgytatatt gtgasgtgag acagcaaaga ccaataaaaa      832
catattttat aagaacaaaa ggcytgggtg cctaccgkg tgggggcacw gtgggaagcc      892
ttctgmtagg gtgtcttggt ctgtrtggyt tgttttgttt gcccyyttat tttgctttgc      952
ttaccagtc ttcccytamt yttggatgst tyttaaccct caggcaaacc tgtgttcccc      1012
ctgtattcag gstytgcttt aaagcaagcc atgaggctgt tggagtttct gtttagggca      1072
ttaaaaattc ccgcaaacta taaagagcaa tgttttcagt yttttaggat tagaagaatt      1132
acataaaaat taataaacat tttcaatgat ggaaaaaaaaaaaa      1176
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<210> 43

<211> 648

<212> DNA

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 460..555

<223> Von Heijne matrix

score 4

seq FSFMLLGMGGCLP/GF

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<220>
<221> polyA_signal
<222> 614..619
<220>
<221> polyA_site
<222> 635..648
<400> 43
aattctggcc cagcttcttc cccagctcta tcttgcttcc ctccatctcc tataggattc      60
tccttagagt tctccctcca ttagtagttg tcttagggtc tgtttctggg gagccctgcc      120
taagactcat gctacaagaa gttaaataag tttcccgaag tcacacagct agcctctcat      180
cccttttcta ctgagaggaa gtggaatgca ctccgacaag gataagggtt tattgtgagc      240
tggccttgga attaaaccac caccaacaca cttttggatt atcagaagggt ggaaggagtg      300
caaatgccag ttacgggtgat gcgttcaaca tccttatttc cagtctttat gacgcctttc      360
ctgaatcaca ggtgcattgg ggtgcttcc cctcccagg actcccaccc aactttgtga      420
acacaaccca cttagaggag ttatctcagc acattatga atg ttg ggg acc acg      474
                                     Met Leu Gly Thr Thr
                                     -30
ggc ctc ggg aca cag ggt cct tcc cag cag gct ctg ggc ttt ttc tcc      522
Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala Leu Gly Phe Phe Ser
      -25                      -20                      -15
ttt atg tta ctt gga atg ggc ggg tgc ctg cct gga ttc ctg cta cag      570
Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro Gly Phe Leu Leu Gln
      -10                      -5                      1                      5
cct ccc aat cga tct cct act ttg cct gca tcc acc ttt gcc cat      615
Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser Thr Phe Ala His
      10                      15                      20
taaagtcaat tctccaccca taaaaaaaaa aaa      648

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<210> 44
<211> 1251
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 79..369
<223> Von Heijne matrix
      score 4
      seq RLPLVVSFIASSS/AN
<220>
<221> polyA_signal
<222> 1217..1222
<220>
<221> polyA_site
<222> 1240..1251
<220>
<221> misc_feature
<222> 2..423
<223> homology
      id :AA056667
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<220>
<221> misc_feature
<222> 463..520
<223> homology
      id :AA056667
      est
<220>
<221> misc_feature

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<222> 418..467
<223> homology
      id :AA056667
      est
<220>
<221> misc_feature
<222> 159..636
<223> homology
      id :AA044187
      est
<220>
<221> misc_feature
<222> 629..684
<223> homology
      id :AA044187
      est
<220>
<221> misc_feature
<222> 5..453
<223> homology
      id :AA131958
      est
<220>
<221> misc_feature
<222> 446..494
<223> homology
      id :AA131958
      est
<220>
<221> misc_feature
<222> 14..343
<223> homology
      id :W95957
      est
<220>
<221> misc_feature
<222> 323..467
<223> homology
      id :W95957
      est
<220>
<221> misc_feature
<222> 463..494
<223> homology
      id :W95957
      est
<220>
<221> misc_feature
<222> 14..475
<223> homology
      id :W95790
      est
<220>
<221> misc_feature
<222> 410..876
<223> homology
      id :AA461134
      est

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<220>
<221> misc_feature
<222> 974..1195
<223> homology
      id :AA595195
      est

<220>
<221> misc_feature
<222> 769..982
<223> homology
      id :AA595195
      est

<220>
<221> misc_feature
<222> 1208..1237
<223> homology
      id :AA595195
      est

<220>
<221> misc_feature
<222> 223..522
<223> homology
      id :AA041216
      est

<220>
<221> misc_feature
<222> 518..636
<223> homology
      id :AA041216
      est

<220>
<221> misc_feature
<222> 774..1127
<223> homology
      id :N94607
      est

<220>
<221> misc_feature
<222> 690..765
<223> homology
      id :N94607
      est

<220>
<221> misc_feature
<222> 833..1195
<223> homology
      id :AA076410
      est

<400> 44
aaagtgcacag cggagagaaac caggsagccc agaaacccca ggcgtggaga ttgatcctgc      60
gagagaagggg ggttcattc atg gcg gat gac cta aag cga ttc ttg tat aaa      111
              Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys
              -95                               -90

aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga      159
Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg
-85                               -80                               -75

gat gga gta cct gtt att aaa gtg gca aat gac aat gct cca gag cat      207
Asp Gly Val Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His

```

-70	-65	-60	-55	
gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa	255			
Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln				
-50	-45	-40		
gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat	303			
Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr				
-35	-30	-25		
aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt	351			
Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser				
-20	-15	-10		
ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc cta gaa	399			
Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu				
-5	1	5	10	
aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa att	447			
Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile				
15	20	25		
tct taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca	500			
Ser				
atatcaatcc agcaatcttt agactacaat aatgctttta tccatgtgct caagaaaggg	560			
cccccttttc caacttatac taaagaacta gcatatagat gtaatttata gatagatcag	620			
ttgctatatt ttctggtgta aggtctttct tatttagtga gatctaggga taccacagaa	680			
atggttcagt ctatcacagc tcccatggag ttagtctggt caccagatat ggatgagaga	740			
ttctattcag tggattagaa tcaaaactggt acattgatcc acttgagccg ttaagtgctg	800			
ccaattgtac aatatgcca ggcttgcaga ataaagccaa ctttttattg tgaataataa	860			
taaggacata tttttcttca gattatgttt tatttctttg cattgagtga ggtacataaa	920			
atggcttggt aaaagtaata aaatcagtac aatcactaac ttctctttgt acatattatt	980			
ttgcagtata gatgaatatt actaatcagt ttgattattc tcagagggtg ctgctcttta	1040			
atgaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg taaccaatca	1100			
gtgttttaaat gtttgtgtgt tcttcataaa atttaaatac aattcgttat tctgtttcca	1160			
atgttagtat gtatgtaaac atgatagtag agccattttt ttcatatgtg agtaaaaata	1220			
aaatagtatt tttaaaagta aaaaaaaaaa a	1251			

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<210> 45
<211> 1524
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 160..231
<223> Von Heijne matrix
      score 5.69999980926514
      seq ILGLLGLLGTLVA/ML
<220>
<221> polyA_signal
<222> 1510..1515
<220>
<221> polyA_site
<222> 1506..1519
<220>
<221> misc_feature
<222> 1048..1504
<223> homology
      id :AA552647
      est
<220>
<221> misc_feature
<222> 597..846
<223> homology

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        id :AA345449
    est
<220>
<221> misc_feature
<222> 39..93
<223> homology
        id :AA345449
    est
<220>
<221> misc_feature
<222> 113..149
<223> homology
        id :AA345449
    est
<220>
<221> misc_feature
<222> 98..400
<223> homology
        id :T86266
    est
<220>
<221> misc_feature
<222> 1210..1489
<223> homology
        id :T86158
    est
<220>
<221> misc_feature
<222> 954..983
<223> homology
        id :AA116709
    est
<400> 45
agctgcttgt ggccacccac agacacttgt aaggaggaga gaagtcagcc tggcagagag      60
actctgaaat gassgattag aggtgttcaa ggragcaaag agcttcagcc tgaagacaag      120
ggagcagtcc ctgaagacgc ttctactgag aggtctgcc atg gcc tct ctt ggc      174
                               Met Ala Ser Leu Gly
                               -20
ctc caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca      222
Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr
                               -15                               -10                               -5
ctg gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt      270
Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly
                               1                               5                               10
gcc agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa      318
Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu
                               15                               20                               25
tgt gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc      366
Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr
                               30                               35                               40                               45
ctt ctg ggc ctg ccc gct gac atc cak gct gcc cag gcc atg atg gtg      414
Leu Leu Gly Leu Pro Ala Asp Ile Xaa Ala Ala Gln Ala Met Met Val
                               50                               55                               60
aca tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc      462
Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly
                               65                               70                               75
atg ara tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg      510
Met Xaa Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val

```

80	85	90	
gcg gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc			558
Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe			
95	100	105	
att cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca			606
Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser			
110	115	120	125
cca ctg gtg cct gac agc atg aaa ttt gag att gga gag gct ctt tac			654
Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr			
	130	135	140
ttg ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc			702
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu			
	145	150	155
tgc ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc			750
Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala			
	160	165	170
tac caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa			798
Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln			
	175	180	185
cct ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat			846
Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr			
190	195	200	205
gtg tgaagaacca ggggccagag ctggggggtg gctgggtctg tgaaaaacag			899
Val			
tggacagcac cccgagggcc acaggtgagg gacactacca ctggatcgtg tcagaaggtg			959
ctgctgaggg tagactgact ttggccattg gattgagcaa aggcagaaat gggggctagt			1019
gtaacagcat gcaggttgaa ttgccaaagga tgctcgccat gccagccttt ctgttttctt			1079
caccttgctg ctcccctgcc ctaagtcccc aaccctcaac ttgaaacccc attcccttaa			1139
gccaggamtc agaggatccc tytgccctck ggtttamctg ggactccatc cccaaaccca			1199
ctaatacatat cccactgact gaccctctgt gatcaaagac cctccctctg gctgaggttg			1259
gstytagct cattgctggg gatgggaagg agaagcagtg gctttystgg gcattgctyt			1319
aacctamtty tcaagcttcc ctccaaagaa amtgattggc cctggaacct ccatccact			1379
yttgttatga ctccacagtg tccagamttaa tttgtgcatg aactgaaata aaaccatcct			1439
acggtatyca gggaacagaa agcaggatgc aggatgggag gacaggaagg cagcctggga			1499
catttaaaaa aataaaaaaa aaaaa			1524

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<210> 46
<211> 610
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 106..201
<223> Von Heijne matrix
      score 8.80000019073486
      seq VPMLLLIVGGSFG/LR
<220>
<221> polyA_signal
<222> 577..582
<220>
<221> polyA_site
<222> 598..610
<220>
<221> misc_feature
<222> 68..167
<223> homology
      id :AA531561
      est

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<220>
<221> misc_feature
<222> 166..262
<223> homology
      id :AA531561
      est

<220>
<221> misc_feature
<222> 423..520
<223> homology
      id :AA531561
      est

<220>
<221> misc_feature
<222> 518..564
<223> homology
      id :AA531561
      est

<220>
<221> misc_feature
<222> 276..313
<223> homology
      id :AA531561
      est

<220>
<221> misc_feature
<222> 41..70
<223> homology
      id :AA531561
      est

<220>
<221> misc_feature
<222> 41..262
<223> homology
      id :AA535454
      est

<220>
<221> misc_feature
<222> 423..520
<223> homology
      id :AA535454
      est

<220>
<221> misc_feature
<222> 518..564
<223> homology
      id :AA535454
      est

<220>
<221> misc_feature
<222> 276..313
<223> homology
      id :AA535454
      est

<220>
<221> misc_feature
<222> 46..262
<223> homology

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        id :H81225
        est
<220>
<221> misc_feature
<222> 2..39
<223> homology
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        est
<220>
<221> misc_feature
<222> 455..493
<223> homology
        id :H81225
        est
<220>
<221> misc_feature
<222> 276..313
<223> homology
        id :H81225
        est
<220>
<221> misc_feature
<222> 423..458
<223> homology
        id :H81225
        est
<220>
<221> misc_feature
<222> 53..262
<223> homology
        id :AA044291
        est
<220>
<221> misc_feature
<222> 423..520
<223> homology
        id :AA044291
        est
<220>
<221> misc_feature
<222> 518..564
<223> homology
        id :AA044291
        est
<220>
<221> misc_feature
<222> 276..313
<223> homology
        id :AA044291
        est
<220>
<221> misc_feature
<222> 125..262
<223> homology
        id :W47031
        est
<400> 46
aaagtgagtt aaggacgtac tcgtcttggt gagagcgtga stgctgagat ttgggagtct

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60

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gcgctaggcc cgcttggagt tctgagccga tggaagagtt cactc atg ttt gca ccc 117
                                Met Phe Ala Pro
                                -30
gcg gtg atg cgt gct ttt cgc aag aac aag act ctc ggc tat gga gtc 165
Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val
-25 -20 -15
ccc atg ttg ttg ctg att gtt gga ggt tct ttt ggt ctt cgt gag ttt 213
Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe
-10 -5 1
tct caa atc cga tat gat gct gtg aag agt aaa atg gat cct gag ctt 261
Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu
5 10 15 20
gaa aaa aaa ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag 309
Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu
25 30 35
gga agt atc tgt tgaagggcta ctatctttcc ttggcccttc tcccttggtg 361
Gly Ser Ile Cys
40
ggactcaatc tccagactat ctccccagag aatcttgatc aggcttggct ttaagctttg 421
ttgggaaaat caaagactcc aagtttgatg actggaagaa tattcgagga ccaggcctt 481
gggaagatcc tgacctcctc caaggaagaa atccaggaaa gccttaagac taagacaact 541
tgactctgct gattcttttt tccttttttt ttttaaataa aaatactatt aactggaaaa 601
aaaaaaaaa 610

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<210> 47
<211> 1370
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 359..466
<223> Von Heijne matrix
      score 7.80000019073486
      seq LTFLFLHLPPSTS/LF
<220>
<221> polyA_signal
<222> 1334..1339
<220>
<221> polyA_site
<222> 1357..1370
<220>
<221> misc_feature
<222> 113..420
<223> homology
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<220>
<221> misc_feature
<222> 406..482
<223> homology
      id :R79290
      est
<220>
<221> misc_feature
<222> 199..420
<223> homology
      id :R81173
      est

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<220>
<221> misc_feature
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<223> homology
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      est

<220>
<221> misc_feature
<222> 2..269
<223> homology
      id :R81277
      est

<220>
<221> misc_feature
<222> 406..646
<223> homology
      id :R74123
      est

<220>
<221> misc_feature
<222> 647..682
<223> homology
      id :R74123
      est

<220>
<221> misc_feature
<222> 439..646
<223> homology
      id :AA450228
      est

<220>
<221> misc_feature
<222> 647..739
<223> homology
      id :AA450228
      est

<220>
<221> misc_feature
<222> 406..646
<223> homology
      id :R02473
      est

<220>
<221> misc_feature
<222> 406..604
<223> homology
      id :T71107
      est

<220>
<221> misc_feature
<222> 71..282
<223> homology
      id :C06030
      est

<220>
<221> misc_feature
<222> 319..365
<223> homology

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        id :C06030
        est
<220>
<221> misc_feature
<222> 2..57
<223> homology
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        est
<220>
<221> misc_feature
<222> 1173..1277
<223> homology
        id :N54909
        est
<220>
<221> misc_feature
<222> 1080..1177
<223> homology
        id :N54909
        est
<220>
<221> misc_feature
<222> 1273..1356
<223> homology
        id :N54909
        est
<220>
<221> misc_feature
<222> 1173..1277
<223> homology
        id :AA196824
        est
<220>
<221> misc_feature
<222> 1080..1177
<223> homology
        id :AA196824
        est
<220>
<221> misc_feature
<222> 1273..1356
<223> homology
        id :AA196824
        est
<400> 47
acaaggcaga gcttctgaat ttcaggcctt cattccagag ccctcttgtg gccaggcctt      60
ccttttgctgg aggaaggtac acagggtgaa gctgawgstg tacttggggg atctccttgg      120
cctgttccac caagtgagag aaggtactta ctcttgtagc tcctgttcag ccagggtgcat      180
taacagacct ccctacagct gtaggaacta ctgtcccaga gctgaggcaa ggggatttct      240
caggtcattt ggagaacaag tgcttttagta gtagtttaaa gtagtaactg ctactgtatt      300
tagtgggggtg gaattcagaa gaaatttgaa gaccagatca tgggtggtct gcatgtga      358
atg aac ach ttt gag cca gac agc ctg gct gtc att gct ttc ttc ctc      406
Met Asn Thr Phe Glu Pro Asp Ser Leu Ala Val Ile Ala Phe Phe Leu
      -35                -30                -25
ccc att tgg acc ttc tct gcc ctt aca ttt ttg ttt ctc cat cta cca      454
Pro Ile Trp Thr Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro
      -20                -15                -10                -5
cca tcc acc agt cta ttt att aac tta gca aga gga caa ata aag ggc      502

```

Pro	Ser	Thr	Ser	Leu	Phe	Ile	Asn	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Gly	
				1				5					10			
cct	ctt	ggc	ttg	att	ttg	ctt	ctt	tct	ttc	tgt	gga	gga	tat	act	aag	550
Pro	Leu	Gly	Leu	Ile	Leu	Leu	Leu	Ser	Phe	Cys	Gly	Gly	Tyr	Thr	Lys	
		15						20					25			
tgc	gac	ttt	gcc	cta	tcc	tat	ttg	gaa	atc	cct	aac	aga	att	gag	ttt	598
Cys	Asp	Phe	Ala	Leu	Ser	Tyr	Leu	Glu	Ile	Pro	Asn	Arg	Ile	Glu	Phe	
	30					35					40					
tct	att	atg	gat	cca	aaa	aga	aaa	aca	aaa	tgc	taatgaagcc	atcasgtcaa				651
Ser	Ile	Met	Asp	Pro	Lys	Arg	Lys	Thr	Lys	Cys						
	45				50				55							
gggtcacatg	ccaataaaca	ataaattttc	cagaagaaat	gaaatccaac	tagacaaata											711
aagtagagct	tatgaaatgg	ttcagtaagg	atgagcttgt	tgttttttgt	tttgttttgt											771
tttgtttttt	taaagacgga	gtctcgctct	gtcactcagg	ctggagtgca	gtggtatgat											831
cttggtctac	tgtaacctcc	gcctcccggg	ttcaagccat	tctcctgcct	cagtctcctg											891
agtagctggg	attgcaggtg	cgtgccacca	tgcttggtta	attttttgtg	ttttggtaga											951
gacagggttt	caccacgttg	gtcgggctgg	tctcgggctc	ctgacctctt	gatccgctg											1011
ccttggcctc	ccaaagtgat	gggattacag	atgtgagcca	ccgtgcctag	ccaaggatga											1071
gatttttaaa	gtatgttcca	gttctgtgtc	atgggttgaa	gacagagtag	gaaggatatg											1131
gaaaagggtca	tggggaagca	gaggtgattc	atggctctgt	ggaatttgag	gtgaatgggt											1191
ccttattgtc	taggccactt	gtgaagaata	tgagtcagtt	attgccagcc	ttggaattta											1251
cttctctagc	ttacaatgga	ccttttttgaa	ctgggaaaca	ccttgtctgc	attcacttta											1311
aaatgtcaaa	actaattttt	ataataaatg	tttattttca	catygaaaaa	aaaaaaaaa											1370

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<210> 48
<211> 791
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 191..286
<223> Von Heijne matrix
      score 8.80000019073486
      seq VPMLLLIVGGSFG/LR
<220>
<221> polyA_signal
<222> 755..760
<220>
<221> polyA_site
<222> 780..791
<220>
<221> misc_feature
<222> 361..531
<223> homology
      id :W73841
      est
<220>
<221> misc_feature
<222> 210..347
<223> homology
      id :W73841
      est
<220>
<221> misc_feature
<222> 548..637
<223> homology
      id :W73841
      est

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<220>
<221> misc_feature
<222> 181..210
<223> homology
      id :W73841
      est

<220>
<221> misc_feature
<222> 361..530
<223> homology
      id :HSU74317
      est

<220>
<221> misc_feature
<222> 238..347
<223> homology
      id :HSU74317
      est

<220>
<221> misc_feature
<222> 568..637
<223> homology
      id :HSU74317
      est

<220>
<221> misc_feature
<222> 698..733
<223> homology
      id :HSU74317
      est

<220>
<221> misc_feature
<222> 361..531
<223> homology
      id :W47031
      est

<220>
<221> misc_feature
<222> 210..347
<223> homology
      id :W47031
      est

<220>
<221> misc_feature
<222> 148..210
<223> homology
      id :W47031
      est

<220>
<221> misc_feature
<222> 548..600
<223> homology
      id :W47031
      est

<220>
<221> misc_feature
<222> 129..347
<223> homology

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        id :AA044118
    est
<220>
<221> misc_feature
<222> 437..531
<223> homology
        id :AA044118
    est
<220>
<221> misc_feature
<222> 361..454
<223> homology
        id :AA044118
    est
<220>
<221> misc_feature
<222> 176..347
<223> homology
        id :AA293342
    est
<220>
<221> misc_feature
<222> 361..531
<223> homology
        id :AA293342
    est
<220>
<221> misc_feature
<222> 548..605
<223> homology
        id :AA293342
    est
<220>
<221> misc_feature
<222> 361..531
<223> homology
        id :AA531561
    est
<220>
<221> misc_feature
<222> 153..252
<223> homology
        id :AA531561
    est
<220>
<221> misc_feature
<222> 750
<223> n=a, g, c or t
<400> 48
aacaagtatg ttacgatggc tcgattgctt ttgcctagcg gaaaccattc actaaggacc      60
gagcaccaaa taaccaagga aaaggaagtg agttaaggac gtactcgtct tggtgagagc      120
gtgagctgct gagatttggg agtctgcgct aggcccgctt ggagttctga gccgatggaa      180
gagttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac          229
          Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
                -30                -25                -20
aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt          277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
          -15                -10                -5

```



tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag	325
Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys	
1 5 10	
ggt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata	373
Gly Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile	
15 20 25	
tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac	421
Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp	
30 35 40 45	
tgg aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc	469
Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu	
50 55 60	
caa gga aga aat cca gaa agc ctt aag act aag aca act tgactctgct	518
Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr	
65 70	
gattctctttt tccttttttt ttttaaataa aaatactatt aactggactt cctaatatat	578
acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg ggtaatttgg	638
atggacaaaa ktaatctktc actaaagggtc atgtaccagg tttttatact tcccagctaa	698
ttccatctgt ggatgaaagt tgcaatgttg gcccccgat katttttacac cntcgaaata	758
aaaaatgtga ataactgctc caaaaaaaaaaaa aaa	791

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<210> 49
<211> 1433
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 346..408
<223> Von Heijne matrix
      score 5.5
      seq SFLPSALVIWTS/AF
<220>
<221> polyA_signal
<222> 1400..1405
<220>
<221> polyA_site
<222> 1420..1433
<220>
<221> misc_feature
<222> 268..634
<223> homology
      id :W02860
      est
<220>
<221> misc_feature
<222> 118..564
<223> homology
      id :N27248
      est
<220>
<221> misc_feature
<222> 268..697
<223> homology
      id :N44490
      est
<220>
<221> misc_feature
<222> 582..687

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<223> homology
      id :AA274731
      est
<220>
<221> misc_feature
<222> 65..369
<223> homology
      id :H94779
      est
<220>
<221> misc_feature
<222> 471..519
<223> homology
      id :H94779
      est
<220>
<221> misc_feature
<222> 61..399
<223> homology
      id :H09880
      est
<220>
<221> misc_feature
<222> 408..452
<223> homology
      id :H09880
      est
<220>
<221> misc_feature
<222> 484..699
<223> homology
      id :H04537
      est
<220>
<221> misc_feature
<222> 685..772
<223> homology
      id :H04537
      est
<220>
<221> misc_feature
<222> 454..486
<223> homology
      id :H04537
      est
<220>
<221> misc_feature
<222> 410..439
<223> homology
      id :H04537
      est
<220>
<221> misc_feature
<222> 572..687
<223> homology
      id :AA466632
      est
<220>

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<221> misc_feature
<222> 260..444
<223> homology
      id :AA459511
      est
<220>
<221> misc_feature
<222> 449..567
<223> homology
      id :AA459511
      est
<220>
<221> misc_feature
<222> 117..184
<223> homology
      id :AA459511
      est
<220>
<221> misc_feature
<222> 260..464
<223> homology
      id :H57434
      est
<220>
<221> misc_feature
<222> 118..184
<223> homology
      id :H57434
      est
<220>
<221> misc_feature
<222> 56..113
<223> homology
      id :H57434
      est
<220>
<221> misc_feature
<222> 454..485
<223> homology
      id :H57434
      est
<220>
<221> misc_feature
<222> 115,1177,1181,1200,1210,1245,1254,1263
<223> n=a, g, c or t
<400> 49
actccttttta gcataggggc ttcggcgcca gcggccagcg ctagtcggtc tggtaagtgc      60
ctgatgccga gttccgtctc tcgcgtcttt tcctggtccc aggcaaagcg gasgnagatc      120
ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cgggtctaatt aattcctctg      180
gtttgttgaa gcagttacca agaatcttca accctttccc acaaaaagcta attgagtaca      240
cgttcctggt gagtacacgt tcctggtgat ttacaaaagg tgcaggatg agcaggctctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                         Met Trp Trp Phe
                                         -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15              -10              -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453

```

Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr	Leu	His	His	Ile	
1					5					10					15	
gac	ccg	gct	tta	cct	tat	atc	agt	gac	act	ggt	aca	gta	gct	cca	gaa	501
Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	Val	Ala	Pro	Glu	
			20					25						30		
aaa	tgc	tta	ttt	ggg	gca	atg	cta	aat	att	gcg	gca	gtt	tta	tgc	att	549
Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	Val	Leu	Cys	Ile	
			35					40						45		
gct	acc	att	tat	gtt	cgt	tat	aag	caa	gtt	cat	gct	ctg	agt	cct	gaa	597
Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala	Leu	Ser	Pro	Glu	
			50				55							60		
gag	aac	gtt	atc	atc	aaa	tta	aac	aag	gct	ggc	ctt	gta	ctt	gga	ata	645
Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly	Ile	
			65				70							75		
ctg	agt	tgt	tta	gga	ctt	tct	att	gtg	gca	aac	ttc	cag	gaa	aac	aac	693
Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Glu	Asn	Asn	
80							85								95	
cct	ttt	tgc	tgc	aca	tgt	aag	tgg	agc	tgt	gct	tac	ctt	tgg	tat	ggg	741
Pro	Phe	Cys	Cys	Thr	Cys	Lys	Trp	Ser	Cys	Ala	Tyr	Leu	Trp	Tyr	Gly	
				100				105						110		
ctc	att	ata	tat	gtt	tgt	tca	gac	cat	cct	ttc	cta	cca	aaa	tgc	agc	789
Leu	Ile	Ile	Tyr	Val	Cys	Ser	Asp	His	Pro	Phe	Leu	Pro	Lys	Cys	Ser	
			115					120						125		
cca	aaa	tcc	aat	ggc	aaa	aca	agt	ctt	ctg	gat	cag	act	gtt	gtt	ggt	837
Pro	Lys	Ser	Asn	Gly	Lys	Thr	Ser	Leu	Leu	Asp	Gln	Thr	Val	Val	Gly	
			130				135							140		
tat	ctg	gtg	tgg	agt	aag	tgc	act	tagcatgctg	acttgctcat	cagttttgca						891
Tyr	Leu	Val	Trp	Ser	Lys	Cys	Thr									
			145				150									
cagtggcaat	tttgggactg	atttagaaca	gaaactccat	tggaaccccg	aggacaaagg											951
ttatgcgctt	cacatgatca	ctactgcagc	agaatggtct	atgtcatttt	ccttctttgg											1011
ttttttcctg	acttacattc	gtgattttca	gaaaattttcc	ttacgggtgg	aagccaactt											1071
acatggatta	accctctatg	acactgcacc	ttgccctatt	aacaatgaac	gaacacggct											1131
actttccags	aagatattag	atgaaaggat	aaaatatttc	tgtaantgan	ttastgastt											1191
ctcagggant	tggggaaaang	gttcacagaa	gttgcttavn	tcttcacrt	gaanattttc											1251
aanccactta	antcaaggct	gacagstaac	acgtgatgaa	tgctgataat	caggaaacat											1311
gaaagaagcc	atttgcatag	attatttytaa	aggatatcat	caagaagamt	attaaaaaca											1371
cctatgccta	tactttttta	tytcagaaaa	taaagtcaaa	agactatgaa	aaaaaaaaaa											1431
aa																1433

```

<210> 50
<211> 1158
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 214..339
<223> Von Heijne matrix
      score 6.09999990463257
      seq AILLQLSQAYWA/LP
<220>
<221> polyA_signal
<222> 1133..1138
<220>
<221> polyA_site
<222> 1146..1158
<220>
<221> misc_feature

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<222> 840..968
<223> homology
      id :H64717
      est
<220>
<221> misc_feature
<222> 858..968
<223> homology
      id :H65208
      est
<220>
<221> misc_feature
<222> 652
<223> n=a, g, c or t
<400> 50
aarttgagct tggggactgc agctgtgggg agatttcagt gcattgcctc ccctgggtgc      60
tcttcacatt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcatcctgs    120
tgrsagtgtg mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct    180
aacagtccat gtgggtgatt cagctctgat ggg atg tgt ttt cca gag cac aga      234
                               Met Cys Phe Pro Glu His Arg
                               -40
aga caa atg tat att caa gat aga ctg gac tct gtc acc agg aga gca      282
Arg Gln Met Tyr Ile Gln Asp Arg Leu Asp Ser Val Thr Arg Arg Ala
-35                               -30                               -25                               -20
cgc caa gga cga ata tgt gct ata cta tta ctc caa tct cag tgt gcc      330
Arg Gln Gly Arg Ile Cys Ala Ile Leu Leu Leu Gln Ser Gln Cys Ala
                               -15                               -10                               -5
tat tgg gcg ctt cca gaa ccg cgt aca ctt gat ggg gga cat ctt atg      378
Tyr Trp Ala Leu Pro Glu Pro Arg Thr Leu Asp Gly Gly His Leu Met
                               1                               5                               10
caa tgatggctct ctctgtctcc aagatgtgca agaggctgac cagggaacct      431
Gln
atatctgtga aatccgcctc aaaggggaga gccaggtggt caagaaggcg gtggtactgc      491
atgtgcttcc agaggagccc aaaggtacgc aaatgcttac ttaaagaggg gccaaggggc      551
aagagctttc atgtgcaaga ggcaaggaaa ctgattatct tgagtaaata ccagcctttg      611
ggctaagtac ttaccacaga gtgaatcttc aaagaaatga ntcattaaat tatttcagrt      671
cagaataaaa atakgagtta ttttagttaa kaataaaaata ttgataatta ttgtattatt      731
actttaaaaca cacttcccc cacaataaagc cctgtgaagg atgttttggt cacatataat      791
gtccaaatat gttttggaca catatttatt aaatggaata aatagtamtt gaaccctggc      851
accthtgaca acaaagtcya tgttyttttt actatgccct aataccttts atcagttatc      911
cacattgatg ctacatytgt attttatagg taccctatgt taggtgtttt gggggataga      971
aaagaaataa gcagkycagg ctacagtggct catgcctgta atcctagcat tttgggaggc    1031
tgaggcagca gaamtgcctg agccccaggg ttcaagactg cagtgagcta tgawggcacc    1091
actgcattyt agcctgggwg acagagcaag actygtttta aaataaaaaa agagaaaaaa    1151
aaaaaaaaa
1158

<210> 51
<211> 850
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 372..437
<223> Von Heijne matrix
      score 6.09999990463257
      seq LFLTCLFWPLAAL/NV
<220>
<221> polyA_signal

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<222> 812..817
<220>
<221> polyA_site
<222> 838..850
<220>
<221> misc_feature
<222> 128..424
<223> homology
      id :N78012
      est
<220>
<221> misc_feature
<222> 61..128
<223> homology
      id :N78012
      est
<220>
<221> misc_feature
<222> 483..554
<223> homology
      id :N78012
      est
<220>
<221> misc_feature
<222> 417..464
<223> homology
      id :N78012
      est
<220>
<221> misc_feature
<222> 460..500
<223> homology
      id :N78012
      est
<220>
<221> misc_feature
<222> 577..612
<223> homology
      id :N78012
      est
<220>
<221> misc_feature
<222> 612..649
<223> homology
      id :N78012
      est
<220>
<221> misc_feature
<222> 546..577
<223> homology
      id :N78012
      est
<220>
<221> misc_feature
<222> 29..63
<223> homology
      id :N78012
      est

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<220>
<221> misc_feature
<222> 128..294
<223> homology
      id :W37233
      est

<220>
<221> misc_feature
<222> 370..509
<223> homology
      id :W37233
      est

<220>
<221> misc_feature
<222> 505..591
<223> homology
      id :W37233
      est

<220>
<221> misc_feature
<222> 293..330
<223> homology
      id :W37233
      est

<220>
<221> misc_feature
<222> 22..57
<223> homology
      id :W37233
      est

<220>
<221> misc_feature
<222> 95..128
<223> homology
      id :W37233
      est

<220>
<221> misc_feature
<222> 128..326
<223> homology
      id :AA186399
      est

<220>
<221> misc_feature
<222> 418..605
<223> homology
      id :AA186399
      est

<220>
<221> misc_feature
<222> 326..423
<223> homology
      id :AA186399
      est

<220>
<221> misc_feature
<222> 39..128
<223> homology

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id :AA186399
est
<220>
<221> misc_feature
<222> 206..640
<223> homology
      id :W52489
      est
<400> 51
agacacttcc tgggtgggatc cgagtgaggc gacggggtag gggttggcgc tcaggcggcg      60
accatggcgt atcacggcct cactgtgcct ctcattgtga tgagcgtgtt ctggggcttc      120
gtcggccttc ttggtgcctt ggttcatccc taagggtcct aaccggggag ttatcattac      180
catgttggtg acctgttcag tttgctgcta tctcttttgg ctgattgcaa ttctggccca      240
actcaaccct ctctttggac cgcaattgaa aaatgaaacc atctggtatc tgaagtatca      300
ttggccttga ggaagaagac atgctctaca gtgctcagtc tttgaggtca cgagaagaga      360
atgccttcta g atg caa aat cac ctc caa acc aga cca ctt ttc ttg act      410
      Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr
      -20 -15 -10
tgc ctg ttt tgg cca tta gct gcc tta aac gtt aac agc aca ttt gaa      458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu
      -5 1 5
tgc ctt att cta caa tgc agc gtg ttt tcc ttt gcc ttt ttt gca ctt      506
Cys Leu Ile Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu
      10 15 20
tgg tgaattacgt gcctccataa cctgaactgt gccgactcca caaaacgatt      559
Trp
atgtactctt ctgagataga agatgctgtt cttctgagag atacgttact ctctccttgg      619
aatctgtgga tttgaaaatg gctcctgcct tctcacgtgg gaatcagtga agtgtttaga      679
aactgctgca agacaaacaa gactccagtg ggggtggtcag taggaaaaca cgttcagagg      739
gaagaaccat ctcaacagaa tcgcaccaa ctatactttc aggatgaatt tcttctttct      799
gccatctttt ggaataaata ttttcctcct ttytatgtaa aaaaaaaaaa a      850

<210> 52
<211> 1107
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 132..215
<223> Von Heijne matrix
      score 3.59999990463257
      seq PLSDSWALLPASA/GV
<220>
<221> polyA_signal
<222> 1069..1074
<220>
<221> polyA_site
<222> 1094..1107
<220>
<221> misc_feature
<222> 177..392
<223> homology
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      est
<220>
<221> misc_feature
<222> 425..542
<223> homology

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<223> homology
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<220>
<221> misc_feature
<222> 113..165
<223> homology
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<220>
<221> misc_feature
<222> 551..590
<223> homology
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<220>
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<222> 166..314
<223> homology
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<222> 27..181
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<220>
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<223> homology
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<220>
<221> misc_feature
<222> 387..441
<223> homology
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<220>
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<221> misc_feature

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<222> 549..580
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<220>
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<223> homology
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      est
<220>
<221> misc_feature
<222> 576..605
<223> homology
      id :AA126732
      est
<220>
<221> misc_feature
<222> 387..477
<223> homology
      id :AA161280
      est
<220>
<221> misc_feature
<222> 292..362
<223> homology
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      est
<220>
<221> misc_feature
<222> 46..113
<223> homology
      id :AA161280
      est
<220>
<221> misc_feature
<222> 217..277
<223> homology
      id :AA161280
      est
<220>
<221> misc_feature
<222> 113..160
<223> homology
      id :AA161280
      est
<220>
<221> misc_feature
<222> 173..217
<223> homology
      id :AA161280
      est
<400> 52
aacaacttcc ggccccactg agcgggtgtcc tgagccgatt acagctaggt agtggagcgc      60
cgctgcttac ctgggtgcag gagacagccg gagtcgctgg gggagctccg cgccgccgga      120
cgcccgtagac c atg tgg agg ctg ctg gct cgc gct agt gcg ccg ctc ctg      170
          Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
          -25                               -20

```

cg	gt	cc	tt	tc	ga	tc	tg	gc	ct	ct	cc	gc	ag	gc	gg	218
Arg	Val	Pro	Leu	Ser	Asp	Ser	Trp	Ala	Leu	Leu	Pro	Ala	Ser	Ala	Gly	
-15					-10					-5					1	
gt	aa	ac	ct	ct	cc	gt	cc	ag	tt	ga	ga	gt	tc	at	cc	266
Val	Lys	Thr	Leu	Leu	Pro	Val	Pro	Ser	Phe	Glu	Asp	Val	Ser	Ile	Pro	
	5						10					15				
ga	aa	cc	aa	ct	ag	tt	at	ga	ag	gc	cc	ct	gt	cc	aa	314
Glu	Lys	Pro	Lys	Leu	Arg	Phe	Ile	Glu	Arg	Ala	Pro	Leu	Val	Pro	Lys	
	20						25					30				
gt	ag	ag	ga	cc	aa	aa	tt	ag	ga	at	cg	gg	cc	tc	ac	362
Val	Arg	Arg	Glu	Pro	Lys	Asn	Leu	Ser	Asp	Ile	Arg	Gly	Pro	Ser	Thr	
	35					40					45					
ga	gc	ac	ga	kk	ac	ga	gg	aa	tt	gc	at	tt	gc	tt	gg	410
Glu	Ala	Thr	Glu	Xaa	Thr	Glu	Gly	Asn	Phe	Ala	Ile	Leu	Ala	Leu	Gly	
50					55				60						65	
gg	gg	ta	ct	ca	tg	gg	ca	tt	ga	at	at	cg	ct	ac	at	458
Gly	Gly	Tyr	Leu	His	Trp	Gly	His	Phe	Glu	Met	Met	Arg	Leu	Thr	Ile	
				70				75						80		
aa	cg	tc	at	ga	cc	aa	aa	at	tt	gc	at	tg	cg	gt	cc	506
Asn	Arg	Ser	Met	Asp	Pro	Lys	Asn	Met	Phe	Ala	Ile	Trp	Arg	Val	Pro	
			85				90					95				
gc	cc	tc	aa	cc	at	ac	cg	aa	ag	gt	gg	ca	cg	at	gg	554
Ala	Pro	Phe	Lys	Pro	Ile	Thr	Arg	Lys	Ser	Val	Gly	His	Arg	Met	Gly	
		100					105					110				
gg	gg	aa	gg	gc	at	ga	ca	ta	gt	ac	cc	gt	aa	gc	gg	602
Gly	Gly	Lys	Gly	Ala	Ile	Asp	His	Tyr	Val	Thr	Pro	Val	Lys	Ala	Gly	
	115					120					125					
cg	mw	gw	gt	ga	at	gg	gg	cg	tg	gm	tt	ga	ga	gt	ca	650
Arg	Xaa	Xaa	Val	Glu	Met	Gly	Gly	Arg	Cys	Xaa	Phe	Glu	Glu	Val	Gln	
	130				135				140						145	
gg	tc	ct	ga	ca	gt	gc	ca	aa	tg	cc	ty	gc	gc	aa	gc	698
Gly	Phe	Leu	Asp	Gln	Val	Ala	His	Lys	Leu	Pro	Phe	Ala	Ala	Lys	Ala	
			150					155						160		
gt	ag	cg	gg	ac	yt	ga	aa	at	cg	aa	ga	ca	ga	ga	ag	746
Val	Ser	Arg	Gly	Thr	Leu	Glu	Lys	Met	Arg	Lys	Asp	Gln	Glu	Glu	Arg	
			165					170				175				
ga	mg	aa	aa	ca	aa	cc	tg	ac	tt	ga	cg	at	gc	ac	gc	794
Glu	Xaa	Asn	Asn	Gln	Asn	Pro	Trp	Thr	Phe	Glu	Arg	Ile	Ala	Thr	Ala	
	180						185					190				
ma	at	ct	gg	at	cg	aa	gt	ct	ag	cc	ta	ga	tg	ac	ca	842
Xaa	Met	Leu	Gly	Ile	Arg	Lys	Val	Leu	Ser	Pro	Tyr	Asp	Leu	Thr	His	
	195					200					205					
aa	gg	aa	ta	tg	gg	aa	ty	ta	at	cc	ma	cg	gt			884
Lys	Gly	Lys	Xaa	Trp	Gly	Lys	Phe	Tyr	Met	Pro	Xaa	Arg	Val			
210					215					220						
ta	gt	ga	gt	ag	ga	ta	ac	tg	ta	ta	ta	ag	st	ac	ta	944
ccc	ct	ca	gc	ta	cc	ca	ct	ga	ag	ty	tt	gg	ta	gc	ty	1004
ttt	ga	ta	ga	ta	ta	ta	ta	ta	ta	ta	ta	ta	ta	ta	ta	1064
at	ta	aa	ta	aa	ta	aa	ta	aa	ta	aa	ta	aa	ta	aa	ta	1107

<210> 53

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 199..288

<223> Von Heijne matrix

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score 5.59999990463257
seq IVSVLALIPETTT/LT
<220>
<221> polyA_signal
<222> 464..469
<220>
<221> polyA_site
<222> 489..500
<220>
<221> misc_feature
<222> 197..412
<223> homology
      id :AA429945
      est
<220>
<221> misc_feature
<222> 61..195
<223> homology
      id :AA429945
      est
<220>
<221> misc_feature
<222> 425..488
<223> homology
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      est
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<221> misc_feature
<222> 197..412
<223> homology
      id :AA455042
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<221> misc_feature
<222> 61..195
<223> homology
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<220>
<221> misc_feature
<222> 425..488
<223> homology
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<220>
<221> misc_feature
<222> 207..412
<223> homology
      id :W93646
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<220>
<221> misc_feature
<222> 58..195
<223> homology
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      est
<220>
<221> misc_feature

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<222> 425..488
<223> homology
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<220>
<221> misc_feature
<222> 197..412
<223> homology
      id :AA516431
      est
<220>
<221> misc_feature
<222> 90..195
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      est
<220>
<221> misc_feature
<222> 425..488
<223> homology
      id :AA516431
      est
<220>
<221> misc_feature
<222> 52..195
<223> homology
      id :W38899
      est
<220>
<221> misc_feature
<222> 197..324
<223> homology
      id :W38899
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<220>
<221> misc_feature
<222> 443..477
<223> homology
      id :W38899
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<220>
<221> misc_feature
<222> 197..338
<223> homology
      id :W52820
      est
<220>
<221> misc_feature
<222> 71..195
<223> homology
      id :W52820
      est
<220>
<221> misc_feature
<222> 339..401
<223> homology
      id :W52820
      est

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<220>
<221> misc_feature
<222> 425..469
<223> homology
      id :W52820
      est

<220>
<221> misc_feature
<222> 40..195
<223> homology
      id :W19506
      est

<220>
<221> misc_feature
<222> 9..10,12
<223> n=a, g, c or t
<400> 53
agagctgtnn cnsaagtagg ggagggcggt gctccgcgm gmgtggcggdh tgctatcgct      60
tcgcagaacc tactcaggca gccagctgag aagagttgag ggaaagtgct gctgctgggt      120
ctgcagacgc gatggataac gtgcagccga aaataaaaaca tcgccccttc tgcttcagtg      180
tgaaaggcca cgtgayag atg ctg cgg ctg gat att atc aac tca ctg gta      231
                Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val
                -30                -25                -20
aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa      279
Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu
                -15                -10                -5
acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca      327
Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala
                1                5                10
gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc      375
Val Cys Cys Leu Ala Asp Gln Ala Leu Ile Tyr Arg Lys Leu Leu Phe
                15                20                25
aat ccc agc ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa      423
Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
                30                35                40                45
gtt ttg taattttata ttacttttta gtttgatact aagtattaaa catatttctg      479
Val Leu
tattcttcca aaaaaaaaaa a      500

<210> 54
<211> 765
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 293..385
<223> Von Heijne matrix
      score 4.40000009536743
      seq TCCHLGLPHPVRA/PR

<220>
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<222> 733..738
<220>
<221> polyA_site
<222> 752..765
<220>
<221> misc_feature
<222> 310..576

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<223> homology
      id :HUM426A07B
      est
<220>
<221> misc_feature
<222> 119
<223> n=a, g, c or t
<400> 54
aaaccttggt gctagggacc gggcggtttg cggcaaccgt gggcactgct gaatttgaat      60
tgaggggcga gggaaaaagt ttcctcaggt gtggtgggga gagggaggcg gatgccgng      120
aaaccgtagg kacgcggtca gaaaggcgac gggctgtcgg agttggaaag ggacgcctgg      180
tttcccccca agcgaaccgg gatgggaagt gacttcaatg agattgaact tcagctggat      240
tgaaagagag gctagaagtt ccgcttgcca gcagcctcct tagtagagcg ga atg agt      298
                                         Met Ser
                                         -30
aat acc cac acg gtg ctt gtc tca ctt ccc cat ccg cac ccg gcc ctc      346
Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro Ala Leu
      -25                                -20                                -15
acc tgc tgt cac ctc ggc ctc cca cac ccg gtc cgc gct ccc cgc cct      394
Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro Arg Pro
      -10                                -5                                1
ctt cct cgc gta gaa ccg tgg gat cct agg tgg cag gac tca gag cta      442
Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser Glu Leu
      5                                10                                15
agg tat cca cag gcc atg aat tcc ttc cta aat gag cgg tca tcg ccg      490
Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser Ser Pro
      20                                25                                30                                35
tgc agg acc tta agg caa gaa gca tcg gct gac aga tgt gat ctc      535
Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp Leu
      40                                45                                50
tgaacctgat agattgctga ttttatctta ttttatcctt gacttggtac aagttttggg      595
attttctgaaa agaccataca gataaccaca aatatcaaga aagtcgtctt cagtattaag      655
tagaatntag atttaggttt ccttcctgct tcccacctcc ttcgaataag gaaacgtctt      715
tgggaccaac tttatggaat aaataagctg agctgcaaaa waaaaaaaaa      765

<210> 55
<211> 584
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 130..189
<223> Von Heijne matrix
      score 3.5
      seq KFCLICLLTFIFH/HC
<220>
<221> polyA_signal
<222> 546..551
<220>
<221> polyA_site
<222> 572..584
<400> 55
aagacgcgcc ggttttctgc acgcagttag cgcagctctgc tttggtgaat acacgatttg      60
gtgcagccgg ggtttggtac cgagcgggaga ggagatgcac acggcactcg agtgtgagga      120
aaaatagaa atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt ttg      171
      Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu
      -20                                -15                                -10
ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat gac      219

```

Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp	
-5 1 5 10	
cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa ttg	267
His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu	
15 20 25	
gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa tac	315
Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr	
30 35 40	
tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta tcc	363
Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser	
45 50 55	
ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag aga	411
Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg	
60 65 70	
aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt tct	459
Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser	
75 80 85 90	
cat tta agg tat ttt ggc agt tca aga ggg aaa gca ttt tca ctc aca	507
His Leu Arg Tyr Phe Gly Ser Ser Arg Gly Lys Ala Phe Ser Leu Thr	
95 100 105	
taaccaccca gcattcccat aatcatttaa attcagaaaa tcaaaactgt gaccagtgtgta	567
wtccacaaaa aaaaaaa	584

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<210> 56
<211> 1387
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 191..325
<223> Von Heijne matrix
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      seq VLVYLVTAERVWS/DD
<220>
<221> polyA_signal
<222> 1348..1353
<220>
<221> polyA_site
<222> 1374..1387
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
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      est
<220>
<221> misc_feature
<222> 791..887
<223> homology
      id :AA417826
      est
<220>
<221> misc_feature
<222> 94..524
<223> homology
      id :AA235826
      est
<220>

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<221> misc_feature
<222> 44..94
<223> homology
      id :AA235826
      est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA236941
      est
<220>
<221> misc_feature
<222> 935..1279
<223> homology
      id :AA480326
      est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
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<220>
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<222> 724..1148
<223> homology
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<220>
<221> misc_feature
<222> 944..1279
<223> homology
      id :AA479344
      est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA479344
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<220>
<221> misc_feature
<222> 1070..1212
<223> homology
      id :AA133636
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<221> misc_feature
<222> 1258..1372
<223> homology
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<220>
<221> misc_feature
<222> 938..1054
<223> homology
      id :AA133636

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      est
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<221> misc_feature
<222> 94..436
<223> homology
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<220>
<221> misc_feature
<222> 32..94
<223> homology
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      est
<220>
<221> misc_feature
<222> 895..1273
<223> homology
      id :AA479453
      est
<220>
<221> misc_feature
<222> 1258..1371
<223> homology
      id :AA253214
      est
<220>
<221> misc_feature
<222> 94..268
<223> homology
      id :AA482378
      est
<220>
<221> misc_feature
<222> 946
<223> n=a, g, c or t
<400> 56
actcccaggc tgggccagca caccggcag gctctgtcct ggaaacaggc ttcaacgggc      60
ttccccgaaa accttccccg cttctggata tgaavattca agctgcttgc tgagtcctat      120
tgccggctgc tgggagccag gagagccctg aggagtagtc actcagtagc agctgacgcg      180
tgggtccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc      229
      Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val
      -45              -40              -35
aac aag tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc      277
Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe
      -30              -25              -20
atc ttc cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt      325
Ile Phe Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser
      -15              -10              -5
gat gac cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc      373
Asp Asp His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser
1              5              10              15
aac gtc tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg      421
Asn Val Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp
      20              25              30
gcc ctg cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg      469
Ala Leu Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met
      35              40              45
cac gtg gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat      517

```

His Val Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His	
50 55 60	
ggg gag aac agt ggg cgc ctc tac ctg aac ccc ggc aag aar cgg ggt	565
Gly Glu Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly	
65 70 75 80	
ggg ctc tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg	613
Gly Leu Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val	
85 90 95	
gac atc gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc	661
Asp Ile Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile	
100 105 110	
ctc cct cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg	709
Leu Pro Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val	
115 120 125	
gac tgc ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc	757
Asp Cys Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe	
130 135 140	
atg gtg gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc	805
Met Val Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu	
145 150 155 160	
atc tac ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa	853
Ile Tyr Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys	
165 170 175	
gct caa gcc atg kgc aca ggt cat cac ccc cav gat acc acy ttt tcc	901
Ala Gln Ala Met Xaa Thr Gly His His Pro Xaa Asp Thr Thr Phe Ser	
180 185 190	
kgc aaa caa gas gac ytc ytt tcg ggk gac ytc atc ttt ctg ggn tca	949
Xaa Lys Gln Xaa Asp Xaa Xaa Ser Gly Asp Xaa Ile Phe Leu Gly Ser	
195 200 205	
gac agt cat cyt cct ytc tta cca gac cgc ccc cga gac cat gtg aag	997
Asp Ser His Xaa Pro Xaa Leu Pro Asp Arg Pro Arg Asp His Val Lys	
210 215 220	
aaa acc aty ttg tgaggggctg cctggamtgg tytggcaggt tgggcctgga	1049
Lys Thr Ile Leu	
225	
tgggggaggct ytagcatyty tcataggtgc aacctgagag tgggggagct aagccatgag	1109
gtagggggcag gcaagagaga ggattcagac gytytgggag ccagttccta gtcctcaamt	1169
ccagccacct gccccagsth gacggcamtg ggccagttcc ccctytgsty tgcagstcgg	1229
tttcctttty tagaatggaa atagtgaggg ccaatgccca gggttggagg gaggagggcg	1289
ttcatagaag aacacacatg cgggcacctt catygtgtgt ggccactgt cagaacttaa	1349
taaaagtcaa mtcatttgct ggttaaaaaa aaaaaaaa	1387

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<222> 141..251

<223> Von Heijne matrix

score 4

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<221> polyA\_site

<222> 1375..1385

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gaagccaggg aagcagtgca atg gct tca aaa atc ttg ctt aac gta caa gag      173
                               Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu
                               -35                               -30

gag gtg acc tgt ccc atc tgc ctg gag ctg ttg aca gaa ccc ttg agt      221
Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser
-25                               -20                               -15

cta gac tgt ggc cac agc ctc tgc cga gcc tgc atc act gtg agc aac      269
Leu Asp Cys Gly His Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn
-10                               -5                               1                               5

aag gag gca gtg acc agc atg gga gga aaa agc agc tgt cct gtg tgt      317
Lys Glu Ala Val Thr Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys
10                               15                               20

ggt atc agt tac tca ttt gaa cat cta cag gct aat cag cat cgg gcc      365
Gly Ile Ser Tyr Ser Phe Glu His Leu Gln Ala Asn Gln His Arg Ala
25                               30                               35

aac ata gtg gag aga ctc aag gag gtc aag ttg agc cca gac aat ggg      413
Asn Ile Val Glu Arg Leu Lys Glu Val Lys Leu Ser Pro Asp Asn Gly
40                               45                               50

aag aag aga gat ctc tgt gat cat cat gga gag aaa ctc cta ctc ttc      461
Lys Lys Arg Asp Leu Cys Asp His His Gly Glu Lys Leu Leu Leu Phe
55                               60                               65                               70

tgt aag gag gat agg aaa gtc att tgc tgg ctt tgt gag cgg tct cag      509
Cys Lys Glu Asp Arg Lys Val Ile Cys Trp Leu Cys Glu Arg Ser Gln
75                               80                               85

gag cac cgt ggt cac cac aca ggt cct cac gga gga agt att caa gga      557
Glu His Arg Gly His His Thr Gly Pro His Gly Gly Ser Ile Gln Gly
90                               95                               100

atg tca gga gaa act cca ggc agt cct caa gag gct gaa gaa gga aga      605
Met Ser Gly Glu Thr Pro Gly Ser Pro Gln Glu Ala Glu Glu Gly Arg
105                               110                               115

gga gga agc tgagaagctg gaagctgaca tcagagaaga gaaaacttcc      654

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Gly Gly Ser

120

tggaagtatc	aggtacaaac	tgagagacaa	aggatacaaa	cagaatttga	tcagcttaga	714
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acgctggata	agtttgcaga	ggctgaggat	gagctagttc	agcagaagca	gttggtgaga	834
gagctcatct	cagatgtgga	gtgtcggagt	cagtgggtcaa	caatggagct	gctgcaggac	894
atgagtggaa	tcataaaatg	gagtgaagtc	tgaggagctga	aaaagccaaa	aatgggtttcc	954
aagaaactga	agactgtatt	ccatgctcca	gatctgagta	ggatgctgcr	aatgttttaga	1014
ggaactgaca	gctgtccggt	gctactgggt	ggatgtcaca	ctgaattcag	tcaacctaaa	1074
tttgaatckt	gtcctttcag	aagatcagag	acaagtgata	tctgtgccaa	tttggccttt	1134
tcagtgttat	aattatgggt	tkbttgggt	cccaatattt	btcctsstgg	gaaacattac	1194
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ccccgccata	tgaagtatgt	tgttagaaga	tgtgcaaaty	gtcaaaatbt	ttacacccaa	1314
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<211> 1497

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<222> 1465..1470

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<221> polyA\_site

<222> 1489..1497

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<222> 958..1110

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est

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<222> 1362..1488

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est

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<222> 1202..1312

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<222> 1115..1190

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<222> 598..639
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<220>
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<220>
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<222> 72,93
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gcgattttcc anssagaaga cagagaagga gcnagtgggtc atggaatggg ctgggggtcaa      120
agactgggtg cctgggagct gaggcagcca ccgtttcagc ctggccagcc ctctggaccc      180
cgaggttgga ccctactgtg acacacctac c atg cgg aca ctc ttc aac ctc      232
                                   Met Arg Thr Leu Phe Asn Leu
                                   -15
ctc tgg ctt gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag      280
Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys
-10                               -5                               1
tca gat gcc asa aaa ccg cct caa aga cgc tgc tgg aga aga gtc agt      328
Ser Asp Ala Xaa Lys Pro Pro Gln Arg Arg Cys Trp Arg Arg Val Ser
5                               10                               15                               20
ttt cag ata agc cgg tgc aar acc ggg gtt tgg tgg tgacggacct      374
Phe Gln Ile Ser Arg Cys Lys Thr Gly Val Trp Trp
25                               30
caaagctgag agtgtgggtt ttgagcatcg cagctactgc tcggcaaagg cccgggacag      434
acactttgct ggggatgtac tgggctatgt cactccatgg aacagccatg gctacgatgt      494

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caccaaggtc	tttgggagca	agttcacaca	gatctcaccc	gtctggctgc	agttgaagag	554
acgtggccgt	gagatgtttg	aggtcacggg	cctccacgac	gtggaccaag	ggtggatgcg	614
agctgtcagg	aagcatgcc	agggcctgca	catagtgcct	cggctcctgt	ttgaggactg	674
gacttacgat	gatttccgga	acgtcttaga	cagtgaggat	gagatagagg	agctgagcaa	734
gaccgtggtc	caggtggcaa	agaaccagca	tttcgatggc	ttcgtgggtg	aggtctggaa	794
ccagctgcta	agccagaagc	gcgtgggcct	catccacatg	ctcaccact	tggccgaggc	854
cctgcaccag	gcccggctgc	tggccctcct	ggcatcccg	cctgccatca	cccccgggac	914
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tttcagcctc	atgacctacg	actactctac	agcgcatcag	cctggcccta	atgcaccct	1034
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tcctcctggg	gctcaacttc	tatggatatg	actacgcgac	ctccaaggat	gcccgtgagc	1154
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ggcgttgggg	tctctatytg	ggagctgggc	cagggcctgg	actacttyta	cgacctgcty	1394
taggtgggca	ttgcggcctc	cgcggtggac	gtgttytttt	ytaagccatg	gagtgagtga	1454
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<222> 1558..1570
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<221> misc_feature
<222> 466..968
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<221> misc_feature
<222> 142..664
<223> homology
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<220>
<221> misc_feature
<222> 114..269
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<222> 2..122
<223> homology
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<220>
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<220>
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<220>
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<222> 92..122
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<220>
<221> misc_feature
<222> 1220..1409
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      est

<220>
<221> misc_feature
<222> 928..1092
<223> homology
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      est

<220>
<221> misc_feature
<222> 1178..1222
<223> homology
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<220>
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<222> 1220..1545
<223> homology

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<221> misc_feature
<222> 1220..1545
<223> homology
        id :N22990
        est
<220>
<221> misc_feature
<222> 1178..1222
<223> homology
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        est
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<221> misc_feature
<222> 114..325
<223> homology
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        est
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<221> misc_feature
<222> 18..122
<223> homology
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<220>
<221> misc_feature
<222> 135..475
<223> homology
        id :HUMEST5H12
        est
<220>
<221> misc_feature
<222> 1093,1128,1135,1147
<223> n=a, g, c or t
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agggtaggga cttctcccg cgcgacgcgg ctggcaagac tgtttgtgtt gcggggggccg      120
gaacttcaag gtgattttac aacgag atg ctg ctc tcc ata ggg atg ctc atg      173
                               Met Leu Leu Ser Ile Gly Met Leu Met
                               -30
ctg tca gcc aca caa gtc tac acc atc ttg act gtc cag ctc ttt gca      221
Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln Leu Phe Ala
-25                -20                -15                -10
ttc tta aac cta ctg cct gta gaa gca gac att tta gca tat aac ttt      269
Phe Leu Asn Leu Leu Pro Val Glu Ala Asp Ile Leu Ala Tyr Asn Phe
-5                1                5
gaa aat gca tct cag aca ttt gat gac ctc ccc gca ara ttt ggt tat      317
Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Xaa Phe Gly Tyr
10                15                20
aga ctt cca gct gaa ggt tta aag ggt ttt tta att aac tca aaa cca      365

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Arg	Leu	Pro	Ala	Glu	Gly	Leu	Lys	Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro		
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gag	aat	gcc	tgt	gaa	ccc	ata	gtg	cct	cca	cca	gta	aaa	gac	aat	tca	413	
Glu	Asn	Ala	Cys	Glu	Pro	Ile	Val	Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser		
40					45					50					55		
tct	ggc	act	ttc	atc	gtg	tta	att	ara	ara	ctt	gat	tgt	aat	ttt	gat	461	
Ser	Gly	Thr	Phe	Ile	Val	Leu	Ile	Xaa	Xaa	Leu	Asp	Cys	Asn	Phe	Asp		
				60					65					70			
ata	aag	gtt	tta	aat	gca	cag	aga	gca	gga	tac	aag	gca	gcc	ata	gtt	509	
Ile	Lys	Val	Leu	Asn	Ala	Gln	Arg	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val		
			75					80					85				
cac	aat	gtt	gat	tct	gat	gac	ctc	att	agc	atg	gga	tcc	aac	gac	att	557	
His	Asn	Val	Asp	Ser	Asp	Asp	Leu	Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile		
		90					95					100					
gag	gta	cta	aag	aaa	att	gac	att	cca	tct	gtc	ttt	att	ggg	gaa	tca	605	
Glu	Val	Leu	Lys	Lys	Ile	Asp	Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser		
	105					110					115						
tca	gct	agt	tct	ctg	aaa	gat	gaa	ttc	aca	tak	gaa	aaa	ggg	ggc	cac	653	
Ser	Ala	Ser	Ser	Leu	Lys	Asp	Glu	Phe	Thr	Xaa	Glu	Lys	Gly	Gly	His		
	120				125					130					135		
ctt	atc	tta	gtt	cca	gaa	ttt	agt	ctt	cct	ttg	gaa	tac	tac	cta	att	701	
Leu	Ile	Leu	Val	Pro	Glu	Phe	Ser	Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile		
				140					145					150			
ccc	ttc	ctt	atc	atr	gtg	ggc	atc	tgt	ctc	atc	ttg	ata	gtc	att	ttc	749	
Pro	Phe	Leu	Ile	Xaa	Val	Gly	Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe		
			155					160					165				
atg	atc	aca	aaa	ttg	tcc	agg	gat	aga	cat	aga	gct	aga	aga	aac	aga	797	
Met	Ile	Thr	Lys	Leu	Ser	Arg	Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg		
		170					175					180					
ctt	cgt	aaa	gat	caa	ctt	aag	aaa	ctt	cct	gta	cat	aaa	ttc	aag	aaa	845	
Leu	Arg	Lys	Asp	Gln	Leu	Lys	Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys		
	185					190					195						
gga	gat	gag	tat	gat	gta	tgt	gcc	att	tgt	ttg	gat	gag	tat	gaa	gat	893	
Gly	Asp	Glu	Tyr	Asp	Val	Cys	Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp		
	200				205					210					215		
gga	gac	aaa	ctc	aga	atc	ctt	ccc	tgt	tcc	cat	gct	tat	cat	tgc	aag	941	
Gly	Asp	Lys	Leu	Arg	Ile	Leu	Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys		
			220					225						230			
tgt	gta	gac	cct	tgg	cta	act	aaa	acc	aaa	aaa	acc	tgt	cca	gtg	tgc	989	
Cys	Val	Asp	Pro	Trp	Leu	Thr	Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys		
			235					240					245				
agg	caa	aaa	gtt	gtt	cct	tct	caa	ggc	gat	tca	gac	tct	gac	aca	gac	1037	
Arg	Gln	Lys	Val	Val	Pro	Ser	Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp		
		250					255					260					
agt	agt	caa	gaa	gaa	aat	gaa	gtg	aca	gaa	cat	acc	cct	tta	ctg	aga	1085	
Ser	Ser	Gln	Glu	Glu	Asn	Glu	Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg		
	265					270					275						
cct	tta	gnc	ttc	tgt	cag	tgc	cca	rgt	cam	ttt	ggg	gct	tta	ntc	gga	1133	
Pro	Leu	Xaa	Phe	Cys	Gln	Cys	Pro	Xaa	Xaa	Phe	Gly	Ala	Leu	Xaa	Gly		
	280				285					290					295		
ant	ccc	gct	cac	ant	cag	aak	cat	gac	aga	atc	att	cag	act	ast	gag	1181	
Xaa	Pro	Ala	His	Xaa	Gln	Xaa	His	Asp	Arg	Ile	Ile	Gln	Thr	Xaa	Glu		
			300					305						310			
gaa	gac	gac	aat	gaa	gat	act	gac	agt	agt	gat	gca	gaa	gaa			1223	
Glu	Asp	Asp	Asn	Glu	Asp	Thr	Asp	Ser	Ser	Asp	Ala	Glu	Glu				
			315					320					325				
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catagcaaat	actgttttgac	tttcagaaga	tgattgggttt	atttcccttt	aaaatgatta	1343											

ggtatatact gtaatttgat tttttgctcc cttaaaagat ttytgtagaa ataacttatt	1403
tttttagtact ytacagttta atcaaattac tgaaacagga cttttgatyt ggtattttatc	1463
tgccaagaat atacttcatt cactaataat agactggtgc tgtaactcaa gcatcaattc	1523
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<210> 60

<211> 1022

<212> DNA

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<220>

<221> sig\_peptide

<222> 112..237

<223> Von Heijne matrix

score 7.19999980926514

seq ILFSLSFLLVIIT/FP

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agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat	117
	Met Asp

tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt	165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly	
-40 -35 -30 -25	

gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc	213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu	
-20 -15 -10	

tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc	261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys	
-5 1 5	

ttg aag atc att aag gag tat gaa cgt gct gtt gta ttc cgt ctg gga	309
Leu Lys Ile Ile Lys Glu Tyr Glu Arg Ala Val Val Phe Arg Leu Gly	
10 15 20	

cgc atc caa gct gac aaa gcc aag ggg cca ggt ttg atc ctg gtc ctg	357
Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu Val Leu	
25 30 35 40	

cca tgc ata gat gtg ttt gtc aag gtt gac ctc cga aca gtt act tgc	405
Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys	
45 50 55	

aac att cct cca caa gag atc ctc acc aga gac tcc gta act act cag	453
Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln	
60 65 70	

gta gat gga gtt gtc tat tac aga atc tat agt gct gtc tca gca gtg	501
Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val	
75 80 85	

gct aat gtc aac gat gtc cat caa gca aca ttt ctg ctg gct caa acc	549
Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr	
90 95 100	

act ctg aga aat gtc tta ggg aca cag acc ttg tcc cag atc tta gct	597
Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala	
105 110 115 120	

gga cga gaa gag atc gcc cat agc atc cag act tta ctt gat gat gcc	645
Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala	
125 130 135	

acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg gaa atc aaa gat gtt	693
Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val	
140 145 150	
cgg att ccc gtg cag ttg cag aga tcc atg gca gcc gag gct gag gcc	741
Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala	
155 160 165	
acc cgg gaa gcg aga gcc aag gtc ctt gca gct gaa gga gaa atg agt	789
Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Ser	
170 175 180	
gct tcc aaa tcc ctg aag tca gcc tcc atg gtg ctg gct gag tct ccc	837
Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu Ser Pro	
185 190 195 200	
ata gct ctc cag ctg cgc tac ctg cag acc ttg agc acg gta gcc acc	885
Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr	
205 210 215	
gag aag aat tct acg att gtg ttt cct ctg ccc atg aat ata cta gag	933
Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu	
220 225 230	
ggc att ggt ggc gtc agc tat gat aac cac aag aag ctt cca aat aaa	981
Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys	
235 240 245	
gcc tgaggctctc ttgcggtagt cagctaaaaa aaaaaaaaa	1022
Ala	

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<221> polyA_site
<222> 603..615
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<222> 341..574
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<222> 174..332
<223> homology
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<222> 85..171
<223> homology
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<220>
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<222> 88..339
<223> homology
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<220>
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<222> 341..574
<223> homology
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<223> homology
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<223> homology
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<220>
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<222> 341..574
<223> homology

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<222> 344..415
<223> homology
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<222> 400..434
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gatcctgcc aacattgttca tgactttaac aagaaactta cagcctatctt agatcttaac      120
ctggataagt gctatgtgat ccctctgaac acttccattg ttatgccacc cagaaaccta      180
ctggagttac ttattaacat caaggctgga acctatttgc ctcagtccta tctgattc      238
atg agc aca tgg tta tta ctg atc gca ttg aaa aca ttg atc acc tgg      286
Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
-25 -20 -15
gtt tct tta ttt atc gac tgt gtc atg aca agg aaa ctt aca aac tgc      334
Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
-10 -5 1 5
aac gct aga gaa act att aaa ggt att cag aaa cgt gaa gcc agc aat      382
Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
10 15 20

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tgt ttc gca att cgg cat ttt gaa aac aaa ttt gcc gtg gaa act tta	430
Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu	
25 30 35	
att tgt tct tgaacagtca agaaaaaacat tattgaggaa aattaatatc	479
Ile Cys Ser	
40	
acagcataac cccacccttt acattttgtg cagtgattat tttttaaagt cttctttcat	539
gtaagtagca aacagggctt tactatcttt tcatctcatt aattcaatta aaaccattac	599
ccccaaaaaa aaaaaa	615

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<222> 771..776
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<221> polyA_site
<222> 791..804
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<222> 520..790
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<221> misc_feature
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<220>
<221> misc_feature

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<220>
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<223> homology
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<220>
<221> misc_feature
<222> 326..790
<223> homology
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<220>
<221> misc_feature
<222> 515..780
<223> homology
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<221> misc_feature
<222> 325..522
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<222> 350..790
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<222> 186..382
<223> homology
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<222> 61..141
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<222> 426..478
<223> homology
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      est

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<223> homology
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<220>
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<222> 389..790
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<220>
<221> misc_feature
<222> 425..790
<223> homology
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<220>
<221> misc_feature
<222> 186..430
<223> homology
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<220>
<221> misc_feature
<222> 59..132
<223> homology
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      est

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aacagcggggc aggggaaagcc gcgggaaggg tactccaggc gagaggcgga cgcgagtcgt      60
cgtggcgagga aaagtgacta gctccccttc gttgtcagcc agggacgaga acacagccac      120
gctcccaccc ggctgcchaa ggatccctcg gcggcg atg tcg gcc gcc ggt gcc      174
                               Met Ser Ala Ala Gly Ala
                               -60

cga ggc ctg cgg gcc acc tac cac cgg ctc ctc gat aaa gtg gag ctg      222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
-55                               -50                               -45

atg ctg ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc      270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
-40                               -35                               -30

aga aca gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt      318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
-25                               -20                               -15                               -10

gct gga ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct      366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
-5                               1                               5

caa tct gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca      414
Gln Ser Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
10                               15                               20

ctt gta att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt      462
Leu Val Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe
25                               30                               35

gtg ggg gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac      510
Val Gly Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn
40                               45                               50                               55

caa gaa cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc      557

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Gln Glu Leu Lys Ala Lys Ala His Lys

60

tgaacaatct	agatgtggac	aaaaccattg	ggacctagtt	tattatttgg	ttattgataa	617
agcaaagcta	actgtgtggt	tagaaggcac	tgtaactggt	agctagttct	tgattcaata	677
gaaaaatgca	gcaaactttt	aataacagtc	tctctacatg	acttaaggaa	cttatctatg	737
gatattagta	acatttttct	accatttgtc	cgtaataaaa	catacttgct	cgtaaaaaaa	797
aaaaaaa						804

<210> 63

<211> 792

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<213> Homo sapiens

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<221> polyA\_site

<222> 780..792

<220>

<221> misc\_feature

<222> 154..428

<223> homology

id :R22491

est

<220>

<221> misc\_feature

<222> 104..160

<223> homology

id :R22491

est

<220>

<221> misc\_feature

<222> 47..218

<223> homology

id :AA136163

est

<220>

<221> misc\_feature

<222> 265..403

<223> homology

id :AA136163

est

<220>

<221> misc\_feature

<222> 3..40

<223> homology

id :AA136163

est

<220>

<221> misc\_feature

<222> 123..265

<223> homology

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<222> 138..403
<223> homology
        id :AA314807
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<222> 164..403
<223> homology
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<222> 163..385
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<222> 154..403
<223> homology
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<223> homology
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<221> misc_feature
<222> 154..403
<223> homology
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<221> misc_feature
<222> 154..403
<223> homology
      id :AA120322
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<220>
<221> misc_feature
<222> 163..403
<223> homology
      id :W71694
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<220>
<221> misc_feature
<222> 164..385
<223> homology
      id :AA250603
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<220>
<221> misc_feature
<222> 266..403
<223> homology
      id :AA036242
      est
<400> 63
aaggcgggtcg ccgggacacc ccgtgtgtgg caggcggcga asgctctgga gaatcccgga      60
cagccctgct ccctgcagcc aggtgtagtt tcgggagcca ctggggccaa agtgagagtc      120
cagcgggtctt ccagcgcttg ggccacggcg gcggccctgg gagcagaggt ggagcgaccc      180
cattacgcta aag atg aaa ggc tgg ggt tgg ctg gcc ctg ctt ctg ggg      229
          Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly
          -20          -15          -10
gcc ctg ctg gga acc gcc tgg gct cgg agg agc cgg gat ctc cac tgt      277
Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys
          -5          1          5
gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa att gcc cag      325
Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln
          10          15          20
gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg atc aat cca      373
Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro
          25          30          35          40
gat ggc agc cag tca gtg gtg gag gta act gtt act gkt tcc ccc aaa      421
Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys
          45          50          55
aca aaa gta gct cac tct ggc ttt tgg atg aaa att cga ctg ctt aaa      469
Thr Lys Val Ala His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys
          60          65          70
aaa gga cct tgg tct taatagaaaa tgaagraaaa cagactcaga aaaaaagatt      524
Lys Gly Pro Trp Ser
          75
tbggctctgt ctcaawtttg aagaaggctg gcaggcttat tccccaatgc aactttgctt      584
cctggctgca aaccyttaat acytttgttt ctgctgtaga aatttgtag ccaaaacawg      644
ggagtctga twcagcaacc ctttcttcca caatccacca tgactggttt ttaatgtamc      704
acttggggta tacatgcaaa accatccggt cmaaaatctg aatycggagc ttaaaaattt      764
aaaaatgaaa aacchaaaaa aaaaaaaaaa      792

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 <222> 789..794  
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 <221> polyA\_site  
 <222> 820..832  
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 <222> 258..553  
 <223> homology  
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 <222> 258..554  
 <223> homology  
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<222> 258..553
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<222> 119..258
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<222> 552..683
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<221> misc_feature
<222> 684..751
<223> homology
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<222> 742..783
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<221> misc_feature
<222> 364..553
<223> homology
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<222> 552..683
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<220>
<221> misc_feature
<222> 684..751

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<223> homology
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<221> misc_feature
<222> 258..461
<223> homology
      id :AA136163
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<220>
<221> misc_feature
<222> 2..172
<223> homology
      id :AA136163
      est
<220>
<221> misc_feature
<222> 216..258
<223> homology
      id :AA136163
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<220>
<221> misc_feature
<222> 743
<223> n=a, g, c or t
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aggagaatcc cggacagccc tgctccctgc agccaggtgt agtttcggga gccactgggg      60
ccaaagtgag agtccagcgg tcttccagcg cttggggccac ggcggcggcc ctgggagcag      120
aggtggagcg accccattac gctaaaag atg aaa ggc tgg ggt tgg ctg gcc ctg      174
                        Met Lys Gly Trp Gly Trp Leu Ala Leu
                        -20                               -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat      222
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
      -10                               -5                               1                               5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa act aga atg gga      270
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Thr Arg Met Gly
                        10                               15                               20
aat tgc cca ggt gga ccc caa gaa gac cat tca gat ggg atc ttt ccg      318
Asn Cys Pro Gly Gly Pro Gln Glu Asp His Ser Asp Gly Ile Phe Pro
                        25                               30                               35
gat caa tcc aga tgg cag cca gtc agt ggt gga ggt gcc tta tgc ccg      366
Asp Gln Ser Arg Trp Gln Pro Val Ser Gly Gly Gly Ala Leu Cys Pro
                        40                               45                               50
ctc aga ggc cca cct cac aga gct gct gga gga gat atg tgaccggatg      415
Leu Arg Gly Pro Pro His Arg Ala Ala Gly Gly Asp Met
                        55                               60                               65
aaggagtatg gggaacagat tgatccttcc acccatcgca agaactacgt acgtgtagtg      475
ggccggaatg gagaatccag tgaactggac ctacaaggca tccgaatcga ctcagatatt      535
agcggcaccc tcaagbtttg cgtgtgggaa cattgtggag gaatacagagg atgaactcat      595
tgaattcttt tcccagagag ctgacaatgt taaagacaaa ctttcagta agcgaacaga      655
tctttgtgac catgccctgc acatatcggc atgatgagct atgaaccact ggagcagccc      715
acactggctt gatggatcac ccccaggnaa gggaaaatgg tggcaatgcc ttttatatat      775
tatgttttac tgaaattaac tgaaaaatat gaaacaaaaa gtscaaaaaa aaaaaaa      832

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<212> DNA
<213> Homo sapiens

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<222> 156..230
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<222> 706..711
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<221> polyA_site
<222> 709..721
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<222> 351..688
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<222> 274..641
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<222> 261..646
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<220>
<221> misc_feature
<222> 165..474
<223> homology
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<220>
<221> misc_feature
<222> 1..74
<223> homology

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<222> 352..646
<223> homology
        id :N22567
    est
<220>
<221> misc_feature
<222> 299..354
<223> homology
        id :N22567
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<220>
<221> misc_feature
<222> 265..303
<223> homology
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<220>
<221> misc_feature
<222> 30..165
<223> homology
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<220>
<221> misc_feature
<222> 270..349
<223> homology
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<220>
<221> misc_feature
<222> 213..261
<223> homology
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<220>
<221> misc_feature
<222> 165..214
<223> homology
        id :AA186657
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<220>
<221> misc_feature
<222> 346..387
<223> homology
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    est
<220>
<221> misc_feature

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<222> 52..400
<223> homology
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<220>
<221> misc_feature
<222> 398..436
<223> homology
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      est
<220>
<221> misc_feature
<222> 171..316
<223> homology
      id :AA143136
      est
<400> 65
attttggttc cggcctgctc gcmgtccgct ccgtccgccc ttagacctgt tgcccagcat      60
ccctgcagtt cgcggwacag tctctattag agcgcgtgta tagaggcaga kaggagtga      120
gtccacagtt cctctcctcc tagagcctgc cgacc atg ccc gcg ggc gtg ccc      173
                               Met Pro Ala Gly Val Pro
                               -25                               -20
atg tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc      221
Met Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys
                               -15                               -10                               -5
gca ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata      269
Ala Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile
                               1                               5                               10
cct gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga      317
Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly
                               15                               20                               25
ctg aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt      365
Leu Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu
30                               35                               40                               45
aaa taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc      418
Lys
ttaatttatt gcatcaaact acttgtcctt aagcacttag tctaagtcta actgcaagag      478
gaggtgctca gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt      538
tcttgaaaac tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg      598
tttagtcttg aatataacgc gaaatagaat atttgtaagt ctactatatg ggttgtcttt      658
atttcatata aattaagaaa ttatttaaaa actatgaact aggtttcatt aaaaaaaaaa      718
gaa                                                                    721

<210> 66
<211> 531
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 272..397
<223> Von Heijne matrix
      score 4.59999990463257
      seq RIPSLPGSPVCWA/WP
<220>
<221> polyA_signal
<222> 503..508
<220>
<221> polyA_site

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<222> 518..531
<220>
<221> misc_feature
<222> 235..517
<223> homology
      id :AA524403
      est
<220>
<221> misc_feature
<222> 52..208
<223> homology
      id :AA524403
      est
<220>
<221> misc_feature
<222> 259..517
<223> homology
      id :N93600
      est
<220>
<221> misc_feature
<222> 85..207
<223> homology
      id :N93600
      est
<220>
<221> misc_feature
<222> 353..517
<223> homology
      id :AA594610
      est
<220>
<221> misc_feature
<222> 258..363
<223> homology
      id :AA594610
      est
<220>
<221> misc_feature
<222> 105..207
<223> homology
      id :AA594610
      est
<220>
<221> misc_feature
<222> 202..517
<223> homology
      id :AA074748
      est
<220>
<221> misc_feature
<222> 116..153
<223> homology
      id :AA074748
      est
<220>
<221> misc_feature
<222> 167..202

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<223> homology
      id :AA074748
      est
<220>
<221> misc_feature
<222> 258..517
<223> homology
      id :N93603
      est
<220>
<221> misc_feature
<222> 208..251
<223> homology
      id :N93603
      est
<220>
<221> misc_feature
<222> 163..202
<223> homology
      id :N93603
      est
<220>
<221> misc_feature
<222> 90..125
<223> homology
      id :N93603
      est
<220>
<221> misc_feature
<222> 125..363
<223> homology
      id :HSPD04938
      est
<220>
<221> misc_feature
<222> 353..517
<223> homology
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      est
<220>
<221> misc_feature
<222> 28..227
<223> homology
      id :AA074804
      est
<220>
<221> misc_feature
<222> 265..310
<223> homology
      id :AA074804
      est
<220>
<221> misc_feature
<222> 227..263
<223> homology
      id :AA074804
      est
<220>

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<221> misc_feature
<222> 352..385
<223> homology
      id :AA074804
      est
<400> 66
aaaaggaaaag aggtysggag cgctcgcgag atctcggacc acccaacctg aaaggtgctt      60
aggaagttga aaggcccaga ggaggcctcc gggcaaattg cggagctgg accgaccatg      120
ctgctacgag aagagaatgg ctgttgcaat cggcgtcaga gcagctccag tgccggggat      180
tcggacggag agcgcgagga ctcggcggct gacgcgccc gacagcagct agaggcgctg      240
ctcaacaaga ctatgcgcat tcgcatgaca g atg gac gga cac tgg tcg gct      292
                                Met Asp Gly His Trp Ser Ala
                                -40
gct ttc tct gca ctg acc gtg act gca atg tca tcc tgg gct cgg cgc      340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35                                -30                                -25                                -20
agg agt tcc tca agc cgt cgg att cct tct ctg ccg ggg agc ccc gtg      388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
                                -15                                -10                                -5
tgc tgg gcc tgg cca tgg tac ccg gac acc aca tcg ttt cca ttg agg      436
Cys Trp Ala Trp Pro Trp Tyr Pro Asp Thr Thr Ser Phe Pro Leu Arg
                                1                                5                                10
tgc aga ggg aga gtc tgaccgggcc tccgtatctc tgaccacgat ggcgcttacc      491
Cys Arg Gly Arg Val
                                15
tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa      531

<210> 67
<211> 783
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 381..629
<223> Von Heijne matrix
      score 8.60000038146973
      seq LELLTSCSPASA/SQ
<220>
<221> polyA_signal
<222> 736..741
<220>
<221> polyA_site
<222> 770..783
<220>
<221> misc_feature
<222> 207..263
<223> homology
      id :AA357230
      est
<400> 67
agggacttcc ggcctcgcgtg gcgtggacgt ttgtggtggg gcgtggtggt ccgcgctctc      60
agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac      120
ccggggtagg gttttgagcc cgtgggagct gcccacgcg gcctcgtcct gccaacggtc      180
ggatggcgga gacgaaggac gcagcgcaga tgttggtgac cttcaaggat gtggctgtga      240
cctttaccog ggaggagtgg agacagctgg acctggccca gaggacctg taccgagagg      300
tgatcggggt cccaaccag agttggtcca cctgctagag catgggcagg agctgtggat      360
agtgaagaga ggcctctcac atg cta cct gtg cag agt ttc act ctt gtt gcc      413
                                Met Leu Pro Val Gln Ser Phe Thr Leu Val Ala

```

						-80						-75					
cag	gct	gga	gtg	cag	tgg	cgc	cat	ctc	agc	tca	ctg	caa	ctt	ctg	cct		461
Gln	Ala	Gly	Val	Gln	Trp	Arg	His	Leu	Ser	Ser	Leu	Gln	Leu	Leu	Pro		
		-70					-65					-60					
ccc	gag	ttc	aag	gga	ttc	tcc	tgc	ctc	agc	ctc	ccg	agt	agc	tgg	gat		509
Pro	Glu	Phe	Lys	Gly	Phe	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp		
		-55					-50					-45					
tac	agg	cgc	cca	cca	cca	tgc	ccg	gct	ggt	ttt	ttt	gta	ttt	tta	gta		557
Tyr	Arg	Arg	Pro	Pro	Pro	Cys	Pro	Ala	Gly	Phe	Phe	Val	Phe	Leu	Val		
		-40				-35					-30				-25		
gag	acg	ggg	ctt	cac	cat	gtt	ggc	cag	gct	ggt	ctt	gaa	ctc	ttg	acc		605
Glu	Thr	Gly	Leu	His	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Leu	Thr		
				-20				-15							-10		
tca	tgt	agt	cca	ccc	gcc	tct	gcc	tcc	caa	agt	gct	gcg	att	aca	ggc		653
Ser	Cys	Ser	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Ala	Ile	Thr	Gly		
		-5					1				5						
gtg	agc	cac	gtg	ccc	ggc	aaa	aaa	aaa	ctg	ctt	aag	ggt	gaa	aag	aaa		701
Val	Ser	His	Val	Pro	Gly	Lys	Lys	Lys	Leu	Leu	Lys	Val	Glu	Lys	Lys		
		10				15					20						
aat	tta	aga	aaw	ttg	ctg	acg	gra	ata	aaa	acy	taataaaaact	accacccgaa					754
Asn	Leu	Arg	Xaa	Leu	Leu	Thr	Xaa	Ile	Lys	Thr							
		25				30				35							
ggaatgaaaa	aaccaaaaaa	aaaaaaaaa															783

```

<210> 68
<211> 996
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
      score 5.90000009536743
      seq IILGCLALFLLLQ/RK
<220>
<221> polyA_signal
<222> 965..970
<220>
<221> polyA_site
<222> 984..996
<220>
<221> misc_feature
<222> 676..959
<223> homology
      id :AA399103
      est
<220>
<221> misc_feature
<222> 609..679
<223> homology
      id :AA399103
      est
<220>
<221> misc_feature
<222> 225..433
<223> homology
      id :AA398040
      est

```

```

<220>
<221> misc_feature
<222> 433..563
<223> homology
      id :AA398040
      est
<400> 68
aacagttacg aaggagagct gcaaaagtgt cagcagaaag gttgggagtc cgcacaggtt      60
ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg      120
gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc      172
                        Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
                        -20                                -15
ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc      220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
      -10                                -5                                1                                5
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt      268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
                        10                                15                                20
gak ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag      316
Xaa Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
                        25                                30                                35
gta tgt ggt cgt ggc ava cgg ggt ctc cag agg aga caa tgc ttt ctt      364
Val Cys Gly Arg Gly Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu
                        40                                45                                50
ttt taaactttct ttcattgact cttaagtgcg gggctagaac acggggaaca      417
Phe
tacctgcttg cctcaaaacta aaggatctag tcmtytctga aktcctctac tsacrtrtra      477
caacaatatc ctgtgcaaaa ttttgcgaaa gaaatgaaat acaattgcmg cgtgcatcga      537
cattttttgga agtagagatt aacyttcgt atttttactt cmtcgaagtt aagttccaaa      597
tgtgtatgtg ttaagtaaat gttttcagta aytgggaaag ataaagtgt atccaattta      657
agtttgtgaa aatgagtaat tccgtatcca aaytgaggtt aacaccaaag tattgtacaa      717
attgcttgca cagttgggtcc gtacacaata gacaggctyt gtattttttag ctgacgttgt      777
tatttgatga tgatgtactc cattttcamt acggcccga gagamtagta atcctccttg      837
tagtagatgt ttttgtcttg aaagtatctt ttaaagtgt gagcacttta aggaacagac      897
ccttattaat gtyttttaag ttttattcaa tttccagtca caaatatttt atggtatttg      957
attgtytaat aaatttgtat gatattaaaa aaaaaaaaaa      996

<210> 69
<211> 657
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 183..338
<223> Von Heijne matrix
      score 3.79999995231628
      seq VMLETGGLLVSLG/QS
<220>
<221> polyA_signal
<222> 620..625
<220>
<221> polyA_site
<222> 644..657
<220>
<221> misc_feature
<222> 207..263
<223> homology
      id :AA357230

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      est
<400> 69
agggacttcc ggcctcgctg gcgtaggacgt ttgtgggtggg gcggtgttggg ccgcgctctc      60
agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac      120
ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgtcct gccaacggtc      180
gg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag      227
    Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
      -50                -45                -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      275
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
      -35                -30                -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt      323
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
      -20                -15                -10
ctg gtt tca cta ggg caa agc att tgg ctg cat ata aca gaa aac cag      371
Leu Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln
      -5                1                5                10
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag      419
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu
      15                20                25
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag      467
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
      30                35                40
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctggatt      527
gtcctcaggc tggctcctca tagggatgct ggggtgctgca gccttgactg gggcagcagg      587
cccccatggt tcaatccatc ctcccacctt ggaataaatg ctttcttttc acaatgagaa      647
aaaaaaaaaa      657

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```

<210> 70
<211> 416
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
      score 5.90000009536743
      seq IILGCLALFLLLQ/RK
<220>
<221> polyA_signal
<222> 383..388
<220>
<221> polyA_site
<222> 405..416
<220>
<221> misc_feature
<222> 225..316
<223> homology
      id :AA398040

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      est
<400> 70
aacagttacg aaggagagct gcaaaagtgt cagcagaaaag gttgggagtc ccgacaggtt      60
ccgtagccca cagaaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg      120
gaagggtgctg gacaaaaaac atg gaa cta att tcc cca aca gtg att ata atc      172
      Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
      -20                -15
ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc      220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg

```

-10	-5	1	5	
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt				268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe				
10	15	20		
gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag				316
Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys				
25	30	35		
tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg acc ttt				364
Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe				
40	45	50		
gtt act gaa gaa gga agg aat taatgtgttt ctaaaatcca aaaaaaaaaa a				416
Val Thr Glu Glu Gly Arg Asn				
55	60			

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<210> 71
<211> 543
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 129..176
<223> Von Heijne matrix
      score 4.80000019073486
      seq SLFIYIFLTCSNT/SP
<220>
<221> polyA_signal
<222> 513..518
<220>
<221> polyA_site
<222> 530..543
<220>
<221> misc_feature
<222> 264..500
<223> homology
      id :AA534039
      est
<220>
<221> misc_feature
<222> 205..315
<223> homology
      id :T82645
      est
<220>
<221> misc_feature
<222> 295..382
<223> homology
      id :T82645
      est
<220>
<221> misc_feature
<222> 375..405
<223> homology
      id :T82645
      est
<220>
<221> misc_feature
<222> 50
<223> n=a, g, c or t

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<400> 71
actgtcccat tcttccccct acaacacaca cacctttcag gcagggasgn gatgagcttc      60
cagccccaag agtggaggct gccacatcct aacatasgta tctattgaaa aggaagcagt      120
gtgtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca tgt agc      170
      Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser
      -15          -10          -5
aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt ctc ccc      218
Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro
      1          5          10
agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc tgc agg      266
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
      15          20          25          30
cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc ctc cac      314
Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His
      35          40          45
ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc tgg gac      362
Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp
      50          55          60
tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact gtcttccttt      415
Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
      65          70
cccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct cccttgccct      475
ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa gtgaaaaaaaa      535
aaaaaaaaa      543

<210> 72
<211> 605
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 285..341
<223> Von Heijne matrix
      score 5.59999990463257
      seq PTLCVSSSPALWA/AS
<220>
<221> polyA_signal
<222> 575..580
<220>
<221> polyA_site
<222> 592..605
<220>
<221> misc_feature
<222> 53..296
<223> homology
      id :W07033
      est
<220>
<221> misc_feature
<222> 348..432
<223> homology
      id :W07033
      est
<220>
<221> misc_feature
<222> 435..497
<223> homology
      id :W07033

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    est
<220>
<221> misc_feature
<222> 293..337
<223> homology
      id :W07033
    est
<220>
<221> misc_feature
<222> 521..560
<223> homology
      id :W07033
    est
<220>
<221> misc_feature
<222> 489..520
<223> homology
      id :W07033
    est
<220>
<221> misc_feature
<222> 15..337
<223> homology
      id :AA151004
    est
<220>
<221> misc_feature
<222> 348..412
<223> homology
      id :AA151004
    est
<220>
<221> misc_feature
<222> 434..485
<223> homology
      id :AA151004
    est
<220>
<221> misc_feature
<222> 83..324
<223> homology
      id :AA476506
    est
<220>
<221> misc_feature
<222> 347..560
<223> homology
      id :AA476506
    est
<220>
<221> misc_feature
<222> 16..347
<223> homology
      id :W56567
    est
<220>
<221> misc_feature
<222> 350..405

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<223> homology
      id :W56567
      est
<220>
<221> misc_feature
<222> 433..470
<223> homology
      id :W56567
      est
<220>
<221> misc_feature
<222> 15..296
<223> homology
      id :AA147584
      est
<220>
<221> misc_feature
<222> 348..421
<223> homology
      id :AA147584
      est
<220>
<221> misc_feature
<222> 293..337
<223> homology
      id :AA147584
      est
<220>
<221> misc_feature
<222> 419..453
<223> homology
      id :AA147584
      est
<220>
<221> misc_feature
<222> 2..338
<223> homology
      id :AA281959
      est
<220>
<221> misc_feature
<222> 350..432
<223> homology
      id :AA281959
      est
<400> 72
aacgcctwta agacagcgga actaagaaaa gaagaggcct gtggacagaa caatcatgtc      60
tgactccctg gtggtgtgcg aggtagaccc agagctaaca gaaaagctga kgaaattccg      120
cttccgaaaa gagacagaca atgcagccat cataatgaag gtggacaaa accggcagat      180
ggtggtgctg gaggaagaat ttcagaacat ttcccagag gagctcaaaa tggagttgcc      240
ggagagacag cccagggttcg tggtttacag ctacaagtac gtgc atg acg atg gcc      296
                                     Met Thr Met Ala
gag tgt cct acc ctt tgt gtt tca tct tct cca gcc ctg tgg gct gca      344
Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala Leu Trp Ala Ala
-15          -10          -5          1
agc gaa aca aca gat gat gta tgc agg gag taaaaacagg ctggtgcaga      394
Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
          5          10

```

cagcagagct	cacaaagggtg	ttcgaaatcc	gcaccactga	tgacctcact	gaggcctggc	454
tccaagaaaa	gttgtctttc	tttcgttgat	ctctgggctg	gggactgaat	tcctgatgtc	514
tgagtcctca	aggtgactgg	ggacttggaa	cccctaggac	ctgaacaacc	aaggacttta	574
aataaatttt	aaaatgcaaa	aaaaaaaaaa	a			605

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<210> 73
<211> 864
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 136..444
<223> Von Heijne matrix
      score 4.90000009536743
      seq VYAFLGLTAPSGS/KE
<220>
<221> polyA_signal
<222> 835..840
<220>
<221> polyA_site
<222> 851..864
<220>
<221> misc_feature
<222> 222..456
<223> homology
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<220>
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<222> 557..648
<223> homology
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<220>
<221> misc_feature
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<222> 130..456
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<222> 557..716
<223> homology
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<222> 365..456
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<220>
<221> misc_feature
<222> 501..571
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<223> homology
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<222> 222..458
<223> homology
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<222> 501..581
<223> homology
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<222> 587..668
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<222> 130..419
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<222> 557..852
<223> homology
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<220>
<221> misc_feature
<222> 501..571
<223> homology
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<220>
<221> misc_feature
<222> 130..384
<223> homology
    id :T35666
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<400> 73
aaagttctcc ttccaccttc cccacacctt ctctgccaac cgctgtttca gcccctagct    60
ggattccagc cattgctgca gctgctccac agcccttttc aggacccaaa caaccgcagc    120
cgctgttccc caggr atg gtg atc cgt gta tat att gca tct tcc tct ggc    171
               Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
                   -100                               -95
tct aca gcg att aag aag aaa caa caa gat gtg ctt ggt ttc cta gaa    219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
   -90               -85               -80
gcc aac aaa ata gga ttt gaa gaa aaa gat att gca gcc aat gaa gag    267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
   -75               -70               -65               -60
aat cgg aag tgg atg aga gaa aat gta cct gaa aat agt cga cca gcc    315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
                   -55               -50               -45
aca ggt aac ccc ctg cca cct cag att ttc aat gaa agc cag tat cgc    363
Thr Gly Asn Pro Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg
                   -40               -35               -30
ggg gac tat gat gcc ttc ttt gaa gcc aga gaa aat aat gca gtg tat    411
Gly Asp Tyr Asp Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr
                   -25               -20               -15
gcc ttc tta ggc ttg aca gcc cca tct ggt tca aag gaa gca gga agg    459
Ala Phe Leu Gly Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg
                   -10               -5               1               5
tgc aag caa agc agc aag cca tgaaccttga gcactgtgct tttaagcatc    510
Cys Lys Gln Ser Ser Lys Pro
                   10
ctgaaaaatg agtctccatt gctttttataa aatagcagaa ttagctttgc sttcaaaaga    570
aataggstta atgttgaaat aatagattag ttgggttttc acatgcaaac amtcaaatg    630
aatacaaaat taaaatttga acattatggt gattatggtg aggagaatgg gatattaaca    690
taaaattata ttaataagta gatatygtag aaatagtgtt gttacctgcc aagccatcct    750
gtatacacca atgattttac aaagaaaaca cccttccctc cttytgccat tamtatggca    810
acctaagtgt atytgcagct ttacattaaa aaggagaaag agaaaaaaaa aaaa    864

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<210> 74
<211> 1033
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 200..427
<223> Von Heijne matrix
      score 4.69999980926514
      seq LIVYLWVVSFIAS/SS
<220>
<221> polyA_signal
<222> 1001..1006
<220>
<221> polyA_site
<222> 1022..1033
<220>
<221> misc_feature
<222> 55..406
<223> homology
      id :AA056667
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<220>
<221> misc_feature
<222> 397..487
<223> homology
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      est
<220>
<221> misc_feature
<222> 527..584
<223> homology
      id :AA056667
      est
<220>
<221> misc_feature
<222> 482..531
<223> homology
      id :AA056667
      est
<220>
<221> misc_feature
<222> 581..634
<223> homology
      id :AA056667
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<220>
<221> misc_feature
<222> 397..700
<223> homology
      id :AA044187
      est
<220>
<221> misc_feature
<222> 222..406
<223> homology
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<223> homology
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<220>
<221> misc_feature
<222> 68..406
<223> homology
      id :AA131958
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<220>
<221> misc_feature
<222> 397..517
<223> homology
      id :AA131958
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<220>
<221> misc_feature
<222> 510..558
<223> homology
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<221> misc_feature
<222> 77..531
<223> homology
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<220>
<221> misc_feature
<222> 527..558
<223> homology
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<220>
<221> misc_feature
<222> 397..586
<223> homology
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<220>
<221> misc_feature
<222> 286..406
<223> homology
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      est
<220>
<221> misc_feature
<222> 582..700
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<220>
<221> misc_feature
<222> 77..406

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<223> homology
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<220>
<221> misc_feature
<222> 397..539
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<220>
<221> misc_feature
<222> 474..760
<223> homology
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<220>
<221> misc_feature
<222> 788..940
<223> homology
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      est
<400> 74
aagacgaggt catgaatcat gtgacggtgg cttgaggagg aacctgtctt taaagctgtc      60
cctgaagtga cagcggagag aaccaggcag cccagaaacc ccaggcgtgg agattgatcc      120
tgcgagagaa ggggggttcat catggcggat gacctaaagc gattcttgta taaaaagtta      180
ccaagtgttg aagggtctcc atg cca ttg ttg tgt cag ata gag atg gag tac      232
                               Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
                               -75                               -70

ctg tta tta aag tgg caa atg aca atg ctc cag agc atg ctt tgc gac      280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65                               -60                               -55                               -50

ctg gtt tct tat cca ctt ttg ccc ttg caa cag acc aag gaa gca aac      328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn
                               -45                               -40                               -35

ttg gac ttt cca aaa ata aaa gta tca tct gtt act ata aca cct acc      376
Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr
                               -30                               -25                               -20

agg tgg ttc aat tta atc gtt tac ctt tgg gtg gtg agt ttc ata gcc      424
Arg Trp Phe Asn Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala
                               -15                               -10                               -5

agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt      472
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu
      1                               5                               10                               15

gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct      514
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
                               20                               25

taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc      574
agcaatccttt agactacaat aatactttta tccatgtgct caagaaaggg cccctttttc      634
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt      694
ttctgggtgta ggggtctttct tatttagtga gatctaggga taccacagaa atgggttcagt      754
ctatcaacag ctcccatgga gttagtctgg tcacagatat ggatgagaga ttytattcag      814
tggtatcagaa tcaaactggt acattgatcc acttgagccg ttaagtgtcg ccaattgtac      874
aatatgccca ggcttgcaga ataaagccaa ctttttattg tgaataataa taaggacata      934
tttttyttca gattatgttt tatttytttg cattgagtga ggaacataaa atggcttggt      994
aaaagtaata aaatcagtac aatcactaaa aaaaaaaaaa      1033

<210> 75
<211> 499

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<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 68..133
<223> Von Heijne matrix
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<220>
<221> polyA_signal
<222> 472..477
<220>
<221> polyA_site
<222> 490..499
<400> 75
aaacagcagt gcctggtcaa acccagcaac ccttgccag aacttactca cccatcccac      60
tgacacc atg aag cct gtg ctg cct ctc cag ttc ctg gtg gtg ttc tgc      109
      Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys
              -20                      -15                      -10
cta gca ctg cag ctg gtg cct ggg agt ccc aag cag cgt gtt ctg aag      157
Leu Ala Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys
      -5                      1                      5
tat atc ttg gaa cct cca ccc tgc ata tca gca cct gaa aac tgt act      205
Tyr Ile Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr
      10                      15                      20
cac ctg tgt aca atg cag gaa gat tgc gag aaa gga ttt cag tgc tgt      253
His Leu Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys
      25                      30                      35                      40
tcc tcc ttc tgt ggg ata gtc tgt tca tca gaa aca ttt caa aag cgc      301
Ser Ser Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg
      45                      50                      55
aac aga atc aaa cac aag ggc tca gaa gtc atc atg cct gcc aac      346
Asn Arg Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn
      60                      65                      70
tgaggcatat ttcctagatc attttgctc tacgatgttt tttcttggtc cacctttagg      406
aaggatttga gaagcaagaa actggaggcc caatatctaa cctgcaaadc gtttttgagt      466
ttggcaataa aggctaactc accaaaaaaaaaaa aaa      499

<210> 76
<211> 978
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 274..399
<223> Von Heijne matrix
      score 5.19999980926514
      seq LLFDLVCHEFCQS/DD
<220>
<221> polyA_signal
<222> 943..948
<220>
<221> polyA_site
<222> 966..978
<220>
<221> misc_feature
<222> 335..518
<223> homology

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        id :AA206225
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<220>
<221> misc_feature
<222> 225..274
<223> homology
        id :AA206225
    est
<220>
<221> misc_feature
<222> 812..861
<223> homology
        id :AA206225
    est
<220>
<221> misc_feature
<222> 186..224
<223> homology
        id :AA206225
    est
<220>
<221> misc_feature
<222> 708..748
<223> homology
        id :AA206225
    est
<220>
<221> misc_feature
<222> 276..314
<223> homology
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<220>
<221> misc_feature
<222> 146..176
<223> homology
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<221> misc_feature
<222> 879..909
<223> homology
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    est
<220>
<221> misc_feature
<222> 182..518
<223> homology
        id :C15003
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<220>
<221> misc_feature
<222> 708..748
<223> homology
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    est
<220>
<221> misc_feature

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<222> 182..517
<223> homology
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<223> homology
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<220>
<221> misc_feature
<222> 517..595
<223> homology
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      est
<220>
<221> misc_feature
<222> 596..665
<223> homology
      id :HUM00TW170
      est
<220>
<221> misc_feature
<222> 697..748
<223> homology
      id :HUM00TW170
      est
<220>
<221> misc_feature
<222> 805..861
<223> homology
      id :HUM00TW170
      est
<220>
<221> misc_feature
<222> 212..369
<223> homology
      id :HUM169E08B
      est
<220>
<221> misc_feature
<222> 406..493
<223> homology
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      est
<220>
<221> misc_feature
<222> 542..595
<223> homology
      id :HUM00TW112
      est
<220>
<221> misc_feature
<222> 697..748
<223> homology
      id :HUM00TW112
      est

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<400> 76
accaggaaca tccagctatt tatgatagca tttgcttcat tatgtcaagt tcaacaaatg      60
ttgacttgct ggtgaagggtg ggggaggttg tggacaagct ctttgatttg gatgagaaac      120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag      180
tctgaagagc agccagtgtt tcggcttgtg ccctgtatac ttgaagctgc caaacaagta      240
cgttctgaaa atccagaatg gcttgatgtt tac atg cac att tta caa ctg ctt      294
                               Met His Ile Leu Gln Leu Leu
                               -40
act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act      342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr
-35                               -30                               -25                               -20
gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc      390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe
                               -15                               -10                               -5
tgc cag tct gat gat cca gcc atc att ctt caa gaa cag aaa aca gtg      438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Glu Gln Lys Thr Val
                               1                               5                               10
cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act      486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
                               15                               20                               25
gag caa gag tat cta aag ata gaa aaa gta gat ctt cct cta att gac      534
Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu Pro Leu Ile Asp
30                               35                               40                               45
agc ctc att cgg gtc tta caa aat atg gaa cag tgt cag aaa aaa cca      582
Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys Gln Lys Lys Pro
                               50                               55                               60
gag aac tcg gca gga gtc taacacagag gaaactaaaa ggactgattt      630
Glu Asn Ser Ala Gly Val
                               65
aaccaagat gatttccact tgaaaatctt aaaaggatat tgttatggtg aagtttctgt      690
ctaataattt ttcaggcatt aacaaaggag acggtggctc agggagtaaa ggaaggccgt      750
tgagcaaaca gaagtgttcc tctgcaattt caaaarcctt cttctttcta tagcccctgt      810
gggtggaaga ttttattaaa atcctacgtg aagttgataa ggcgcttgct kgatgacttg      870
gaaaaaaamc ttcccaagtt tgaaggttca gaastaaaaa rscktgaatg ggaattactt      930
sstgtbcaag aaaataaact ttatttttct cactgaaaaa aaaaaaaa      978

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<210> 77
<211> 587
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 421..465
<223> Von Heijne matrix
      score 3.90000009536743
      seq LVPLGQSFPLSEP/RC
<220>
<221> polyA_signal
<222> 553..558
<220>
<221> polyA_site
<222> 575..587
<220>
<221> misc_feature
<222> 182..322
<223> homology
      id :T35951
      est

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<220>
<221> misc_feature
<222> 32..132
<223> homology
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      est

<220>
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<222> 136..193
<223> homology
      id :T35951
      est

<220>
<221> misc_feature
<222> 182..322
<223> homology
      id :T35949
      est

<220>
<221> misc_feature
<222> 32..132
<223> homology
      id :T35949
      est

<220>
<221> misc_feature
<222> 136..193
<223> homology
      id :T35949
      est

<220>
<221> misc_feature
<222> 136..299
<223> homology
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      est

<220>
<221> misc_feature
<222> 32..132
<223> homology
      id :AA381111
      est

<220>
<221> misc_feature
<222> 136..322
<223> homology
      id :AA381001
      est

<220>
<221> misc_feature
<222> 85..132
<223> homology
      id :AA381001
      est

<220>
<221> misc_feature
<222> 182..322
<223> homology

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<220>
<221> misc_feature
<222> 136..193
<223> homology
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    est
<220>
<221> misc_feature
<222> 82..132
<223> homology
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    est
<220>
<221> misc_feature
<222> 316..428
<223> homology
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    est
<220>
<221> misc_feature
<222> 475..554
<223> homology
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<220>
<221> misc_feature
<222> 182..322
<223> homology
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<220>
<221> misc_feature
<222> 136..192
<223> homology
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    est
<220>
<221> misc_feature
<222> 41..119
<223> homology
        id :AA090647
    est
<220>
<221> misc_feature
<222> 136..184
<223> homology
        id :AA090647
    est
<220>
<221> misc_feature
<222> 316..426
<223> homology
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aattcatttt tcactcctcc ctccctaggtc acactttttca gaaaaagaat ctgcacccctg

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60

gaaaccagaa gaaaaaatatg agacggggaa tcatcgtgtg atgtgtgtgc tgcctttggc	120
tkwgtgtgk gaagtycckg ctcaggtgtt aggtacagtg tgtttgatcg tgggtggcttg	180
aggggaaccc gctgttcaga gctgtgactg cggctgcact cagagaagct gcccttggct	240
gctcgtacg ccgggccttc tctcctcgtc atcatccaga gcagccagtg tccgggaggc	300
agaagatgcc cactccagc ctctggactg ggggctctct tcagtggctg aatgtccagc	360
agagctatct ccttcacag ggggccttgc aggggaaggt ccaggacttg acatcttaag	420
atg cgt ctt gtc ccc ttg ggc cag tca ttt ccc ctc tct gag cct cgg	468
Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg	
-15 -10 -5 1	
tgt ctt caa cct gtg aaa tgg gat cat aat cac tgc ctt acc tcc ctc	516
Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu	
5 10 15	
acg gtt gtt gtg agg act gag tgt gtg gaa gtt ttt cat aaa ctt tgg	564
Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp	
20 25 30	
atg cta gtg taaaaaaaaa aaaa	587
Met Leu Val	
35	

<210> 78  
 <211> 400  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> sig\_peptide  
 <222> 198..278  
 <223> Von Heijne matrix  
 score 4.90000009536743  
 seq CLLSYIALGAIHA/KI

<220>	
<221> polyA_signal	
<222> 364..369	
<220>	
<221> polyA_site	
<222> 387..400	
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tctgactcca tggaaaccag atggggcaac ggggtgggtc tagtgcagac tgtagctgca	120
gctcctctcc acctctagcc tgctcatttc cagctcagaa attctactaa tggcgttttt	180
tcttcttgaa aaaggaa atg aac agg gtc cct gct gat tct cca aat atg	230
Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met	
-25 -20	
tgt cta atc tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca	278
Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala	
-15 -10 -5	
aaa atc tgt aga aga gca ttc cag gaa gag gga aga gca aat gca aag	326
Lys Ile Cys Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys	
1 5 10 15	
acg ggc gtg aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc	375
Thr Gly Val Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys	
20 25	
ttggaatagc caaaaaaaaaa aaaaa	400

<210> 79  
 <211> 1166  
 <212> DNA  
 <213> Homo sapiens  
 <220>

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<221> sig_peptide
<222> 167..229
<223> Von Heijne matrix
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      seq LVLSLQFLLLSYD/LF
<220>
<221> polyA_signal
<222> 1133..1138
<220>
<221> polyA_site
<222> 1154..1166
<220>
<221> misc_feature
<222> 22..377
<223> homology
      id :AA306911
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<220>
<221> misc_feature
<222> 424..540
<223> homology
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      est
<220>
<221> misc_feature
<222> 376..424
<223> homology
      id :AA306911
      est
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<221> misc_feature
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<222> 225..563
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<220>
<221> misc_feature
<222> 544..631

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<222> 629..660
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<221> misc_feature
<222> 680..793
<223> homology
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<223> n=a, g, c or t
<400> 79
aatgacaacc gacgttggag tttggaggtg cttgccttag agcaagggaa acagctctca      60
ttcaaaggaa ctagaagcct ctccctcagt ggtagggaga cagccaggag cggttttctg      120
ggaactgtgg gatgtgccct tgggggcccg agaaaacaga aggaag atg ctc cag      175
                                         Met Leu Gln
                                         -20
acc agt aac tac agc ctg gtg ctc tct ctg cag ttc ctg ctg ctg tcc      223
Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu Leu Leu Ser
      -15                               -10                               -5
tat gac ctc ttt gtc aat tcc ttc tca gaa ctg ctc caa aag act cct      271
Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln Lys Thr Pro
      1                               5                               10
gtc atc cag ctt gtg ctc ttc atc atc cag gat att gca gtc ctc ttc      319
Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala Val Leu Phe
      15                               20                               25                               30
aac atc atc atc att ttc ctc atg ttc ttc aac acc tcc gtc ttc cag      367
Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser Val Phe Gln
      35                               40                               45
gct ggc ctg gtc aac ctc cta ttc cat aag ttc aaa ggg acc atc atc      415
Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly Thr Ile Ile
      50                               55                               60
ctg aca gct gtg tac ttt gcc ctc agc atc tcc ctt cat gtc tgg gtc      463
Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His Val Trp Val
      65                               70                               75
atg aac tta cgc tgg aaa aac tcc aac agc ttc ata tgg aca gat gga      511
Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp Thr Asp Gly
      80                               85                               90
ctt caa atg ctg ttt gta ttc cag aga cta gca gca gtg ttg tac tgc      559
Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val Leu Tyr Cys
      95                               100                               105                               110
tac ttc tat aaa cgg aca gcc gta aga cta ggc gat cct cac ttc tac      607
Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro His Phe Tyr
      115                               120                               125
cag gac tct ttg tgg ctg cgc aag gag ttc atg caa gtt cga agg      652
Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val Arg Arg
      130                               135                               140
tgacctcttg tcacactgat ggatactttt ccttcctgat agaagccaca tttgctgctt      712
tgcagggaga gttggcccta tgcattgggca aacagctgga ctttccaagg aaggttcaga      772
ctagctgtgt tcagcattca agaaggaaga tccccctct tgcacaatta gagtgtcccc      832

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atcgggtctcc	agtgcggcat	cccttccttg	ccttctacct	ctgttccacc	cccttccttc	892
ctctcctctc	tgtaccattc	attctccctg	accggccttt	cttgccgagg	gttctgtggc	952
tcttaccctt	gtgaagcttt	tccttttagcc	tgggacagaa	ggacctccc	gcccccaaag	1012
gatctccag	wtgaccaaag	gatgcgaaga	gtgatagtta	cgntgctcct	gactgatcac	1072
accgcagaca	tttagatttt	tataccaag	gcactttaa	aaaatgtttt	ataaatagag	1132
aataaattga	attyttgttc	caaaaaaaaa	aaaa			1166

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<222> 722..727
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<221> polyA_site
<222> 743..754
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<221> misc_feature
<222> 116..450
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<220>
<221> misc_feature
<222> 593..710
<223> homology
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<222> 18..117
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<222> 48..511
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<220>
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<222> 392..437
<223> homology
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<220>
<221> misc_feature
<222> 343..511
<223> homology
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<222> 535..710
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<221> misc_feature
<222> 256..341

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<222> 248..511
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<222> 21..271
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<220>
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<222> 121..450
<223> homology
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<220>
<221> misc_feature
<222> 592..710
<223> homology
      id :W68728
      est
<220>
<221> misc_feature
<222> 725
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ggcctgctgg gcttggcaac gagggactcg gcctcggagg cgacccagac cacacagaca      120
ctgggtcaag gagtaagcag aggataaaca actggaagga gagcaagcac aaagtcatac      179
atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt      227
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
      -65                                -60                                -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg      275
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
      -50                                -45                                -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa      323
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
      -35                                -30                                -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt      371
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
      -20                                -15                                -10                                -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga      419
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
      1                                5                                10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc      467
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
      15                                20                                25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt      515
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
      30                                35                                40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt ccw aca gca      557
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala

```



45	50	55	
taacaggcac	tgcctcctta	cctgtgagga	atgcaaaata aagcatggat taagtgagaa 617
gggagactct	cagccttcag	cttcctaaat	tctgtgtctg tgactttcga agtttttttaa 677
acctctgaat	ttgtacacat	ttaaaaatttc	aaggtgtact ttaaaatnaa aatacttcta 737
atgtvaaaaa	aaaaaaaa		754

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<221> polyA_signal
<222> 680..685
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<221> polyA_site
<222> 697..708
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<221> misc_feature
<222> 137..291
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<221> misc_feature
<222> 6..91
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<222> 95..132
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<220>
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<222> 460..501
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<222> 432..465
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<223> homology
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<220>
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<222> 392..658
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<220>
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<222> 271..327
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<223> homology
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<220>
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<222> 312..344
<223> homology
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<223> homology
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<220>
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<222> 150..258
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<220>
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<222> 95..171
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<220>
<221> misc_feature
<222> 322..628
<223> homology

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        id :HSPD02295
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<221> misc_feature
<222> 445..670
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<220>
<221> misc_feature
<222> 2..102
<223> homology
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<220>
<221> misc_feature
<222> 95..171
<223> homology
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<220>
<221> misc_feature
<222> 150..222
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ggcgggagaag ggtgcgggct cttcgccctt tgtgtccttc ttctactaac ttctggactt      120
tccagctctt ccgaagtctg ttcttgcgca aagcccaaag gctggaaaac cgtccacg      178
atg acc agc atg act cag tct ctg cgg gag gtg ata aag gcc atg acc      226
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40                               -35                               -30                               -25
aag gct cgc aat ttt gag aga gtt ttg gga aag att act ctt gtc tct      274
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
-20                               -15                               -10
gct gct cct ggg aaa gtg att tgt gaa atg aaa gta gaa gaa gag cat      322
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
-5                               1                               5
acc aat gca ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta      370
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
10                               15                               20
gat aac ata tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc      418
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25                               30                               35                               40
gga gtc agt gtc gat atg aac ata acg tac atg tca cct gca aaa tta      466
Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
45                               50                               55
gga gag gat ata gtg att aca gca cat gtt ctg aag caa gga aaa aca      514
Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
60                               65                               70
ctt gca ttt acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta      562
Leu Ala Phe Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu
75                               80                               85
ata gca caa gga aga cac aca aaa cac ctg gga aac tgagagaaca      608
Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
90                               95                               100
gcagaatgac ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaaacaatt      668

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gtaatttttg aaataaacta gcaaaaccaa aaaaaaaaaa g

709

<210> 82  
<211> 243  
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<213> Homo sapiens  
<220>  
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<222> 100..171  
<223> Von Heijne matrix  
score 3.70000004768372  
seq ILFNLLIFLCGFT/NY  
<220>  
<221> polyA\_signal  
<222> 211..216  
<220>  
<221> polyA\_site  
<222> 230..243  
<220>  
<221> misc\_feature  
<222> 2..164  
<223> homology  
id :H64488  
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<223> homology  
id :AA131065  
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<222> 5..164  
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id :AA224847  
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est  
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<222> 10..164  
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        id :AA100852
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<222> 79..164
<223> homology
        id :AA146774
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<221> misc_feature
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<223> homology
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<222> 109..164
<223> homology
        id :AA299239
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<222> 158..207
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<221> misc_feature

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<223> homology
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<222> 200..229
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<220>
<221> misc_feature
<222> 200..229
<223> homology
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ttcagaactc actgccaaga gccctgaaca ggagccacc atg cag tgc ttc agc      114
                                   Met Gln Cys Phe Ser
                                   -20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt      162
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
      -15                      -10                      -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg      210
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
      1                      5                      10
cat aaa cct gtt aca atg taaaaaaaaa aaaaaa      243
His Lys Pro Val Thr Met
      15

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<213> Homo sapiens
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<221> sig_peptide
<222> 346..408
<223> Von Heijne matrix
      score 5.5
      seq SFLPSALVIWTS/AF
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<222> 792..797
<220>
<221> polyA_site
<222> 817..829
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<221> misc_feature
<222> 260..464
<223> homology
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<221> misc_feature
<222> 118..184
<223> homology
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<220>
<221> misc_feature
<222> 56..113
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<220>
<221> misc_feature
<222> 454..485
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<221> misc_feature
<222> 118..545
<223> homology
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<222> 393..432

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<220>
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<222> 260..444
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<221> misc_feature
<222> 449..545
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<222> 117..184
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<223> homology
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<220>

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<221> misc_feature
<222> 115
<223> n=a, g, c or t
<400> 83
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ctgatgccga gttccgtctc tcgcgtcttt tcctgggtccc aggcaaagcg gasgnagatc      120
ctcaaacggc ctagtgcttc gcgcttcgag agaaaatcag cgggtctaatt aattcctctg      180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca      240
cgttcctgtt gactacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                     Met Trp Trp Phe
                                     -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                      5                      10                      15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca gaa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu
      20                      25                      30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt caa      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                      40                      45
aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa      602
Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgattt gctttctaca ctgttgaatt      662
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact tggataaata      722
tggttaagggtg ggcttttccc cctgtgtaat tggctacsac gtcttacttg agccaagttg      782
gtaagttgaa ataaaatgat watgagagtg acacavaaaa aaaaaaa      829

<210> 84
<211> 674
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 177..233
<223> Von Heijne matrix
      score 6.09999990463257
      seq LALLWSLPASDLG/RS
<220>
<221> polyA_signal
<222> 644..649
<220>
<221> polyA_site
<222> 663..674
<220>
<221> misc_feature
<222> 194..592
<223> homology
      id :AA496246
      est
<220>
<221> misc_feature
<222> 1..100
<223> homology
      id :AA496246

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    est
<220>
<221> misc_feature
<222> 99..202
<223> homology
      id :AA496246
    est
<220>
<221> misc_feature
<222> 187..592
<223> homology
      id :AA476481
    est
<220>
<221> misc_feature
<222> 594..661
<223> homology
      id :AA476481
    est
<220>
<221> misc_feature
<222> 188..592
<223> homology
      id :AA496245
    est
<220>
<221> misc_feature
<222> 594..661
<223> homology
      id :AA496245
    est
<220>
<221> misc_feature
<222> 194..444
<223> homology
      id :AA476480
    est
<220>
<221> misc_feature
<222> 1..102
<223> homology
      id :AA476480
    est
<220>
<221> misc_feature
<222> 99..187
<223> homology
      id :AA476480
    est
<220>
<221> misc_feature
<222> 437..592
<223> homology
      id :AA505488
    est
<220>
<221> misc_feature
<222> 594..661

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<223> homology
      id :AA505488
      est
<220>
<221> misc_feature
<222> 441..592
<223> homology
      id :AA554685
      est
<220>
<221> misc_feature
<222> 594..661
<223> homology
      id :AA554685
      est
<220>
<221> misc_feature
<222> 414..503
<223> homology
      id :AA215595
      est
<220>
<221> misc_feature
<222> 510..539
<223> homology
      id :AA215595
      est
<400> 84
ataagtgaac cagaccaccc tgatggcatc cacagtgatg tcaaggttgg ggctggccag      60
gggtgggtgg actagaagca tttgggagta gtggccaggg gccctggacg ctagccacgg      120
agctgctgca cagagcctgg tgtccacaag cttccagggt ggggttggag cctggg atg      179
                                   Met
agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct gac      227
Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser Asp
      -15                                -10                                -5
ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt ctc      275
Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val Leu
      1                                5                                10
atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc aag      323
Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr Lys
      15                                20                                25                                30
agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt gta      371
Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val Val
      35                                40                                45
aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca tgagtcgatg      420
Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
      50                                55
ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg tcgaaaataa      480
gcaccttggt aactaaaccc ctctaatagc tataaaggct ttagttctgt attgattaag      540
ttactgtaaa agctttgggtt tattttttgta ggacttaatg gctaagaatt agggaacata      600
gcaagggggc tcctctgttg gagtaatgta aattgtaatt ataaataaac atgcaaacct      660
ttaaaaaaaaa aaaa      674

<210> 85
<211> 478
<212> DNA
<213> Homo sapiens
<220>

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<221> sig_peptide
<222> 179..319
<223> Von Heijne matrix
      score 5.5
      seq SALLFFARPCVFC/FK
<220>
<221> polyA_signal
<222> 461..466
<220>
<221> polyA_site
<222> 465..478
<220>
<221> misc_feature
<222> 2..464
<223> homology
      id :AA310996
      est
<220>
<221> misc_feature
<222> 8..464
<223> homology
      id :AA312901
      est
<220>
<221> misc_feature
<222> 2..416
<223> homology
      id :AA401411
      est
<220>
<221> misc_feature
<222> 2..349
<223> homology
      id :R64030
      est
<220>
<221> misc_feature
<222> 56..464
<223> homology
      id :AA400108
      est
<220>
<221> misc_feature
<222> 126..273
<223> homology
      id :AA010825
      est
<220>
<221> misc_feature
<222> 2..147
<223> homology
      id :AA010825
      est
<220>
<221> misc_feature
<222> 358..435
<223> homology
      id :AA010825

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    est
<220>
<221> misc_feature
<222> 78..464
<223> homology
      id :AA504732
    est
<220>
<221> misc_feature
<222> 90..441
<223> homology
      id :H60506
    est
<220>
<221> misc_feature
<222> 59..349
<223> homology
      id :AA346780
    est
<220>
<221> misc_feature
<222> 2..331
<223> homology
      id :AA281167
    est
<220>
<221> misc_feature
<222> 6..236
<223> homology
      id :R35805
    est
<220>
<221> misc_feature
<222> 232..284
<223> homology
      id :R35805
    est
<220>
<221> misc_feature
<222> 41..307
<223> homology
      id :H13784
    est
<220>
<221> misc_feature
<222> 2..40
<223> homology
      id :H13784
    est
<220>
<221> misc_feature
<222> 64..280
<223> homology
      id :AA128122
    est
<220>
<221> misc_feature
<222> 293..349

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<223> homology
      id :AA128122
      est
<220>
<221> misc_feature
<222> 332..385
<223> homology
      id :AA128122
      est
<220>
<221> misc_feature
<222> 163..420
<223> homology
      id :AA555127
      est
<400> 85
aagtccttcg cgccctcctc gccctcccca cgcacatcat gctccagttc ctgcttggat      60
ttacactggg caacgtggtt ggaatgtatc tggctcagaa ctatgatata ccaaacctgg      120
ctaaaaaact tgaagaaatt aaaaaggact tggatgccaa gaagaaaccc cctagtgc      178
atg aga ctg cct cca gca ctg cct tca gga tat act gat tct act gct      226
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
      -45                -40                -35
ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt tcg tct      274
Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
      -30                -25                -20
cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt tgc ttt      322
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
      -15                -10                -5                1
aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca ttt cca      370
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
      5                10                15
aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg agg ttc      418
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
      20                25                30
taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa aaaaacaaaa      478

<210> 86
<211> 952
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 112..237
<223> Von Heijne matrix
      score 7.19999980926514
      seq ILFSLSFLLVIIT/FP
<220>
<221> polyA_signal
<222> 910..915
<220>
<221> polyA_site
<222> 940..952
<400> 86
aatacttttct cctctccctt ctccaagca catctgagtt gctgcctggt cttcacactt      60
agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat      117
Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt      165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly

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-40	-35	-30	-25	
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc	213			
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu				
-20	-15	-10		
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc	261			
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys				
-5	1	5		
ttg aag att tgatcctggt cctgccatgc ataratgtgt ttgtcaaagt	310			
Leu Lys Ile				
10				
tgacctccga acagttactt gcaacattcc tccacaagag atcctcacca rgagactccg	370			
taactactca ggtagatgga gttgtctatt acagaatcta tagtgctgtc tcagcagtgg	430			
ctaakgtcaa cgatgtccat caagcaacat ttctgctggc tcaaaccact ctgagaaatg	490			
tcktagggac acaggacctt gtccccagat cttaggctgg acgagaagag atcgcccata	550			
agcatccaga ctktacttga tgatgccacc gaactgggtg gggatccggg tggcccgagt	610			
ggaaatcaaa gatgttcgga ttccccgtgca gttgcagaga tccatggcag ccgaggstga	670			
ggccacccgg gaagsgagag ccaaggtcct tgcagctgaa ggagaaatga atgsttccaa	730			
atccctgaag tcagcctcca tgggtgstggs tgagtytccc atagctytcc agstgsgsta	790			
cctgcagacc ttgagcacgg tagccaccga gaagaatttt acgattgtgt ttctbtgcc	850			
catgaatata ctagagggca ttggtggcgt cagstatgat aaccacaaga agsttbscaa	910			
ataaagcctg aggtcybctt gcggtagtca aaaaaaaaaa aa	952			

<210> 87  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -13...-1  
 <400> 87

Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu			
-10	-5	1	
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro			
5	10	15	
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu			
20	25	30	35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile			
40	45	50	
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu			
55	60	65	
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys			
70	75	80	
Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg			
85	90	95	
Gly Arg Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp			
100	105	110	115
Tyr Leu Lys			

<210> 88  
 <211> 63  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -35...-1  
 <400> 88

Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn			
-35	-30	-25	-20

His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys  
                   -15                  -10                  -5  
 Val Phe Ser Leu Lys Gln Leu Lys Lys Lys Ser Trp Ser Lys Tyr Leu  
                   1                  5                  10  
 Phe Glu Ser Cys Cys Tyr Arg Ser Leu Tyr Val Cys Val Phe Ile  
           15                  20                  25

<210> 89  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -31..-1  
 <220>  
 <221> UNSURE  
 <222> 91,108,109,112,124  
 <223> Xaa = any one of the twenty amino acids  
 <400> 89

Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly  
           -30                  -25                  -20  
 Ser Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys  
   -15                  -10                  -5                  1  
 Ser Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn  
                   5                  10                  15  
 Ile Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro  
           20                  25                  30  
 Ser Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys  
   35                  40                  45  
 Pro Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp  
  50                  55                  60                  65  
 Pro Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr  
                   70                  75                  80  
 Ser Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg  
                   85                  90                  95  
 Gly Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys  
           100                  105                  110  
 Gly Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr  
           115                  120                  125  
 Pro Pro Pro  
 130

<210> 90  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -32..-1  
 <400> 90

Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala  
           -30                  -25                  -20  
 Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro  
   -15                  -10                  -5  
 Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser  
  1                  5                  10                  15  
 Thr Phe Ala His  
           20



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<210> 91
<211> 124
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -97..-1
<400> 91
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
      -95                      -90                      -85
Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
      -80                      -75                      -70
Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
      -65                      -60                      -55                      -50
Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
      -45                      -40                      -35
Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
      -30                      -25                      -20
Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
      -15                      -10                      -5
Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
      1                      5                      10                      15
Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile Ser
      20                      25

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<210> 92
<211> 230
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -24..-1
<220>
<221> UNSURE
<222> 54,79
<223> Xaa = any one of the twenty amino acids
<400> 92
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
      -20                      -15                      -10
Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
      -5                      1                      5
Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
      10                      15                      20
Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
      25                      30                      35                      40
Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Xaa Ala Ala
      45                      50                      55
Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
      60                      65                      70
Ile Ser Val Val Gly Met Xaa Cys Thr Val Phe Cys Gln Glu Ser Arg
      75                      80                      85
Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly
      90                      95                      100
Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu
      105                      110                      115                      120
Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile
      125                      130                      135

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Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile  
                   140                  145                  150  
 Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser  
                   155                  160                  165  
 Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser  
                   170                  175                  180  
 Pro Arg Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr  
                   185                  190                  195                  200  
 Ser Leu Thr Gly Tyr Val  
                                   205

<210> 93  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -32..-1  
 <400> 93

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
                   -30                  -25                  -20  
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly  
                   -15                  -10                  -5  
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met  
                   5                  10                  15  
 Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu  
                   20                  25                  30  
 Ser Glu Tyr Glu Gly Ser Ile Cys  
                   35                  40

<210> 94  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -36..-1  
 <400> 94

Met Asn Thr Phe Glu Pro Asp Ser Leu Ala Val Ile Ala Phe Phe Leu  
                   -35                  -30                  -25  
 Pro Ile Trp Thr Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro  
                   -20                  -15                  -10                  -5  
 Pro Ser Thr Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly  
                   1                  5                  10  
 Pro Leu Gly Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys  
                   15                  20                  25  
 Cys Asp Phe Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe  
                   30                  35                  40  
 Ser Ile Met Asp Pro Lys Arg Lys Thr Lys Cys  
                   45                  50                  55

<210> 95  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -32..-1

<400> 95

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
-30 -25 -20  
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly  
-15 -10 -5  
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Gly Lys Met  
1 5 10 15  
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu  
20 25 30  
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn  
35 40 45  
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg  
50 55 60  
Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr  
65 70

<210> 96

<211> 172

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 96

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val  
-20 -15 -10  
Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr  
-5 1 5 10  
Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr  
15 20 25  
Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala  
30 35 40  
Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala  
45 50 55  
Leu Ser Pro Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu  
60 65 70 75  
Val Leu Gly Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe  
80 85 90  
Gln Glu Asn Asn Pro Phe Cys Cys Thr Cys Lys Trp Ser Cys Ala Tyr  
95 100 105  
Leu Trp Tyr Gly Leu Ile Ile Tyr Val Cys Ser Asp His Pro Phe Leu  
110 115 120  
Pro Lys Cys Ser Pro Lys Ser Asn Gly Lys Thr Ser Leu Leu Asp Gln  
125 130 135  
Thr Val Val Gly Tyr Leu Val Trp Ser Lys Cys Thr  
140 145 150

<210> 97

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 97

Met Cys Phe Pro Glu His Arg Arg Gln Met Tyr Ile Gln Asp Arg Leu  
-40 -35 -30  
Asp Ser Val Thr Arg Arg Ala Arg Gln Gly Arg Ile Cys Ala Ile Leu

-25                      -20                      -15  
 Leu Leu Gln Ser Gln Cys Ala Tyr Trp Ala Leu Pro Glu Pro Arg Thr  
 -10                      -5                      1                      5  
 Leu Asp Gly Gly His Leu Met Gln  
                     10

<210> 98  
 <211> 46  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -22..-1  
 <400> 98

Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe  
                     -20                      -15                      -10  
 Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile  
                     -5                      1                      5                      10  
 Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu Trp  
                     15                      20

<210> 99  
 <211> 251  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -28..-1  
 <220>  
 <221> UNSURE  
 <222> 54,131,132,140,179,194,213,221  
 <223> Xaa = any one of the twenty amino acids  
 <400> 99

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro  
                     -25                      -20                      -15  
 Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr  
                     -10                      -5                      1  
 Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro  
 5                      10                      15                      20  
 Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg  
                     25                      30                      35  
 Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr  
                     40                      45                      50  
 Glu Xaa Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr  
                     55                      60                      65  
 Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser  
                     70                      75                      80  
 Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe  
 85                      90                      95                      100  
 Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys  
                     105                      110                      115  
 Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Xaa Xaa  
                     120                      125                      130  
 Val Glu Met Gly Gly Arg Cys Xaa Phe Glu Glu Val Gln Gly Phe Leu  
                     135                      140                      145  
 Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg  
                     150                      155                      160  
 Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Xaa Asn

165		170		175		180									
Asn	Gln	Asn	Pro	Trp	Thr	Phe	Glu	Arg	Ile	Ala	Thr	Ala	Xaa	Met	Leu
				185					190					195	
Gly	Ile	Arg	Lys	Val	Leu	Ser	Pro	Tyr	Asp	Leu	Thr	His	Lys	Gly	Lys
			200					205					210		
Xaa	Trp	Gly	Lys	Phe	Tyr	Met	Pro	Xaa	Arg	Val					
		215					220								

<210> 100  
 <211> 77  
 <212> PRT  
 <213> Homo sapiens  
 <220>

<221> SIGNAL  
 <222> -30..-1  
 <400> 100

Met	Leu	Arg	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe	Met
-30					-25					-20					-15
Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr	Leu	Thr
				-10					-5					1	
Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys	Cys	Leu	Ala
	5						10				15				
Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn	Pro	Ser	Gly	Pro
20					25					30					
Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys	Glu	Val	Leu			
35					40					45					

<210> 101  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens  
 <220>

<221> SIGNAL  
 <222> -31..-1  
 <400> 101

Met	Ser	Asn	Thr	His	Thr	Val	Leu	Val	Ser	Leu	Pro	His	Pro	His	Pro
-30						-25					-20				
Ala	Leu	Thr	Cys	Cys	His	Leu	Gly	Leu	Pro	His	Pro	Val	Arg	Ala	Pro
-15					-10					-5					1
Arg	Pro	Leu	Pro	Arg	Val	Glu	Pro	Trp	Asp	Pro	Arg	Trp	Gln	Asp	Ser
		5					10					15			
Glu	Leu	Arg	Tyr	Pro	Gln	Ala	Met	Asn	Ser	Phe	Leu	Asn	Glu	Arg	Ser
20					25					30					
Ser	Pro	Cys	Arg	Thr	Leu	Arg	Gln	Glu	Ala	Ser	Ala	Asp	Arg	Cys	Asp
35					40					45					

Leu  
 50

<210> 102  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens  
 <220>

<221> SIGNAL  
 <222> -20..-1  
 <400> 102

Met	Lys	Val	His	Met	His	Thr	Lys	Phe	Cys	Leu	Ile	Cys	Leu	Leu	Thr
-20					-15					-10					-5

Phe	Ile	Phe	His	His	Cys	Asn	His	Cys	His	Glu	Glu	His	Asp	His	Gly
				1				5					10		
Pro	Glu	Ala	Leu	His	Arg	Gln	His	Arg	Gly	Met	Thr	Glu	Leu	Glu	Pro
	15						20					25			
Ser	Lys	Phe	Ser	Lys	Gln	Ala	Glu	Asn	Glu	Lys	Lys	Tyr	Tyr	Ile	
	30				35					40					
Glu	Lys	Leu	Phe	Glu	Arg	Tyr	Gly	Glu	Asn	Gly	Arg	Leu	Ser	Phe	Phe
45					50				55					60	
Gly	Leu	Glu	Lys	Leu	Leu	Thr	Asn	Leu	Gly	Leu	Gly	Glu	Arg	Lys	Val
				65				70						75	
Val	Glu	Ile	Asn	His	Glu	Asp	Leu	Gly	His	Asp	His	Val	Ser	His	Leu
			80				85					90			
Arg	Tyr	Phe	Gly	Ser	Ser	Arg	Gly	Lys	Ala	Phe	Ser	Leu	Thr		
	95						100					105			

<210> 103  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -45...-1  
 <220>  
 <221> UNSURE  
 <222> 181,187,193,196,198,199,203,212,214  
 <223> Xaa = any one of the twenty amino acids  
 <400> 103

Met	Asn	Trp	Ser	Ile	Phe	Glu	Gly	Leu	Leu	Ser	Gly	Val	Asn	Lys	Tyr
-45					-40					-35					-30
Ser	Thr	Ala	Phe	Gly	Arg	Ile	Trp	Leu	Ser	Leu	Val	Phe	Ile	Phe	Arg
				-25				-20						-15	
Val	Leu	Val	Tyr	Leu	Val	Thr	Ala	Glu	Arg	Val	Trp	Ser	Asp	Asp	His
			-10					-5					1		
Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser	Asn	Val	Cys
5					10					15					
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
20					25					30				35	
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				40				45						50	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn
			55					60					65		
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp
	70					75						80			
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala
	85				90						95				
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro
100					105					110				115	
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe
				120					125					130	
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala
			135					140					145		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
			150					155				160			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	165					170					175				
Met	Xaa	Thr	Gly	His	His	Pro	Xaa	Asp	Thr	Thr	Phe	Ser	Xaa	Lys	Gln
180					185					190				195	
Xaa	Asp	Xaa	Xaa	Ser	Gly	Asp	Xaa	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His

				200					205					210			
Xaa	Pro	Xaa	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile		
			215					220					225				

Leu

<210> 104  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -37...-1  
 <400> 104

Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro		
		-35					-30					-25					
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His		
	-20					-15					-10						
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr		
-5					1				5					10			
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser		
		15					20					25					
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Arg	Ala	Asn	Ile	Val	Glu	Arg		
	30					35					40						
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu		
45					50					55							
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg		
60				65					70					75			
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His		
			80					85						90			
His	Thr	Gly	Pro	His	Gly	Gly	Ser	Ile	Gln	Gly	Met	Ser	Gly	Glu	Thr		
		95					100					105					
Pro	Gly	Ser	Pro	Gln	Glu	Ala	Glu	Glu	Gly	Arg	Gly	Gly	Ser				
	110						115					120					

<210> 105  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -19...-1  
 <220>  
 <221> UNSURE  
 <222> 8  
 <223> Xaa = any one of the twenty amino acids  
 <400> 105

Met	Arg	Thr	Leu	Phe	Asn	Leu	Leu	Trp	Leu	Ala	Leu	Ala	Cys	Ser	Pro		
			-15					-10					-5				
Val	His	Thr	Thr	Leu	Ser	Lys	Ser	Asp	Ala	Xaa	Lys	Pro	Pro	Gln	Arg		
		1				5					10						
Arg	Cys	Trp	Arg	Arg	Val	Ser	Phe	Gln	Ile	Ser	Arg	Cys	Lys	Thr	Gly		
	15				20						25						
Val	Trp	Trp															
30																	

<210> 106  
 <211> 359  
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34..-1

<220>

<221> UNSURE

<222> 20,64,65,130,156,282,288,289,294,296,300,302,310

<223> Xaa = any one of the twenty amino acids

<400> 106

Met	Leu	Leu	Ser	Ile	Gly	Met	Leu	Met	Leu	Ser	Ala	Thr	Gln	Val	Tyr
				-30					-25					-20	
Thr	Ile	Leu	Thr	Val	Gln	Leu	Phe	Ala	Phe	Leu	Asn	Leu	Leu	Pro	Val
			-15					-10					-5		
Glu	Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	Glu	Asn	Ala	Ser	Gln	Thr	Phe
		1				5					10				
Asp	Asp	Leu	Pro	Ala	Xaa	Phe	Gly	Tyr	Arg	Leu	Pro	Ala	Glu	Gly	Leu
15					20					25					30
Lys	Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	Glu	Asn	Ala	Cys	Glu	Pro	Ile
				35					40					45	
Val	Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Val	Leu
			50				55						60		
Ile	Xaa	Xaa	Leu	Asp	Cys	Asn	Phe	Asp	Ile	Lys	Val	Leu	Asn	Ala	Gln
	65						70					75			
Arg	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	His	Asn	Val	Asp	Ser	Asp	Asp
	80					85					90				
Leu	Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile	Glu	Val	Leu	Lys	Lys	Ile	Asp
95					100					105					110
Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asp
				115					120					125	
Glu	Phe	Thr	Xaa	Glu	Lys	Gly	Gly	His	Leu	Ile	Leu	Val	Pro	Glu	Phe
			130					135					140		
Ser	Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	Pro	Phe	Leu	Ile	Xaa	Val	Gly
		145					150					155			
Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Leu	Ser	Arg
	160					165					170				
Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys
175					180					185					190
Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys
				195					200					205	
Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu
			210					215					220		
Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr
	225						230					235			
Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser
	240					245					250				
Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu
255					260					265					270
Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Xaa	Phe	Cys	Gln	Cys
				275					280					285	
Pro	Xaa	Xaa	Phe	Gly	Ala	Leu	Xaa	Gly	Xaa	Pro	Ala	His	Xaa	Gln	Xaa
			290					295					300		
His	Asp	Arg	Ile	Ile	Gln	Thr	Xaa	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr
	305						310						315		
Asp	Ser	Ser	Asp	Ala	Glu	Glu									
	320					325									

<210> 107

<211> 291



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<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42...-1
<400> 107
Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe
  -40                      -35          -30
Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe
  -25                      -20          -15
Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp
  -10                      -5           1           5
Met Cys Leu Lys Ile Ile Lys Glu Tyr Glu Arg Ala Val Val Phe Arg
      10                      15           20
Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu
      25                      30           35
Val Leu Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val
      40                      45           50
Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr
      55                      60           65           70
Thr Gln Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser
      75                      80           85
Ala Val Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala
      90                      95          100
Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile
      105                     110          115
Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp
      120                     125          130
Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys
      135                     140          145          150
Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala
      155                     160          165
Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu
      170                     175          180
Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu
      185                     190          195
Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val
      200                     205          210
Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile
      215                     220          225          230
Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro
      235                     240          245
Asn Lys Ala

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<210> 108
<211> 67
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -26...-1
<400> 108
Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
  -25                      -20          -15
Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
  -10                      -5           1           5
Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
      10                      15           20

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Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu  
 25 30 35  
 Ile Cys Ser  
 40

<210> 109  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -63...-1  
 <400> 109

Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu  
 -60 -55 -50  
 Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr  
 -45 -40 -35  
 Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met  
 -30 -25 -20  
 Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala  
 -15 -10 -5 1  
 Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe  
 5 10 15  
 Ile Trp Ser Arg Tyr Ser Leu Val Ile Ile Pro Lys Asn Trp Ser Leu  
 20 25 30  
 Phe Ala Val Asn Phe Phe Val Gly Ala Ala Gly Ala Ser Gln Leu Phe  
 35 40 45  
 Arg Ile Trp Arg Tyr Asn Gln Glu Leu Lys Ala Lys Ala His Lys  
 50 55 60

<210> 110  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -20...-1  
 <220>  
 <221> UNSURE  
 <222> 53  
 <223> Xaa = any one of the twenty amino acids  
 <400> 110

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly  
 -20 -15 -10 -5  
 Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys Gly Ala Cys Arg  
 1 5 10  
 Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys  
 15 20 25  
 Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln  
 30 35 40  
 Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys Thr Lys Val Ala  
 45 50 55 60  
 His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys Lys Gly Pro Trp  
 65 70 75  
 Ser

<210> 111  
 <211> 86

<212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -20..-1  
 <400> 111  
 Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly  
 -20 -15 -10 -5  
 Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg  
 1 5 10  
 Ala Leu Val Asp Glu Thr Arg Met Gly Asn Cys Pro Gly Gly Pro Gln  
 15 20 25  
 Glu Asp His Ser Asp Gly Ile Phe Pro Asp Gln Ser Arg Trp Gln Pro  
 30 35 40  
 Val Ser Gly Gly Gly Ala Leu Cys Pro Leu Arg Gly Pro Pro His Arg  
 45 50 55 60  
 Ala Ala Gly Gly Asp Met  
 65

<210> 112  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -25..-1  
 <400> 112  
 Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala  
 -25 -20 -15 -10  
 Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr  
 -5 1 5  
 Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu  
 10 15 20  
 Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val  
 25 30 35  
 Ser Gln Gln Glu Glu Leu Lys  
 40 45

<210> 113  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -42..-1  
 <400> 113  
 Met Asp Gly His Trp Ser Ala Ala Phe Ser Ala Leu Thr Val Thr Ala  
 -40 -35 -30  
 Met Ser Ser Trp Ala Arg Arg Ser Ser Ser Ser Arg Arg Ile Pro  
 -25 -20 -15  
 Ser Leu Pro Gly Ser Pro Val Cys Trp Ala Trp Pro Trp Tyr Pro Asp  
 -10 -5 1 5  
 Thr Thr Ser Phe Pro Leu Arg Cys Arg Gly Arg Val  
 10 15

<210> 114  
 <211> 118  
 <212> PRT

<213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -83...-1  
 <220>  
 <221> UNSURE  
 <222> 28,32  
 <223> Xaa = any one of the twenty amino acids  
 <400> 114  
 Met Leu Pro Val Gln Ser Phe Thr Leu Val Ala Gln Ala Gly Val Gln  
                   -80                  -75                  -70  
 Trp Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro Glu Phe Lys Gly  
                   -65                  -60                  -55  
 Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Arg Pro Pro  
                   -50                  -45                  -40  
 Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu Thr Gly Leu His  
                   -35                  -30                  -25                  -20  
 His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys Ser Pro Pro  
                                   -15                  -10                  -5  
 Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser His Val Pro  
                                   1                  5                  10  
 Gly Lys Lys Lys Leu Leu Lys Val Glu Lys Lys Asn Leu Arg Xaa Leu  
           15                  20                  25  
 Leu Thr Xaa Ile Lys Thr  
 30                  35

<210> 115  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -22...-1  
 <220>  
 <221> UNSURE  
 <222> 22,43  
 <223> Xaa = any one of the twenty amino acids  
 <400> 115  
 Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala  
                   -20                  -15                  -10  
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile  
                   -5                  1                  5                  10  
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Xaa Phe Gly Lys Ala  
                                   15                  20                  25  
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly  
                   30                  35                  40  
 Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe  
           45                  50

<210> 116  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -52...-1  
 <400> 116  
 Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp

-50		-45		-40
Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala				
-35		-30		-25
Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu				
-20		-15		-10
Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile				
	1		5	10
Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys				
15		20		25
Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln				
30		35		40

<210> 117  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -22...-1  
 <400> 117

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala				
-20		-15		-10
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile				
-5		1		5
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala				
	15		20	25
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe				
	30		35	40
Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Gly				
45		50		55
Arg Asn				
60				

<210> 118  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -16...-1  
 <400> 118

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr				
-15		-10		-5
Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala				
1		5		10
Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe				
	20		25	30
Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile				
	35		40	45
Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala				
	50		55	60
Glu Ala Gly Ala Ser Leu Tyr Ser Pro				
65		70		

<210> 119  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19..-1  
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<210> 120  
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 Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile  
                   -85                  -80                  -75  
 Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp  
                   -70                  -65                  -60  
 Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro  
                   -55                  -50                  -45                  -40  
 Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp  
                   -35                  -30                  -25  
 Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly  
                   -20                  -15                  -10  
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 Ser Lys Pro  
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<210> 121  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens  
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 <222> -76..-1  
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 Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro  
                   -60                  -55                  -50                  -45  
 Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys  
                   -40                  -35                  -30  
 Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Asn Leu  
                   -25                  -20                  -15  
 Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser Ala Asn  
                   -10                  -5                  1  
 Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu  
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 Glu Leu Arg Gln Val Val Glu Val Ser  
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<210> 122

<211> 93  
 <212> PRT  
 <213> Homo sapiens  
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 <222> -22...-1  
 <400> 122  
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 Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys Tyr Ile  
           -5                  1                  5                  10  
 Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr His Leu  
                   15                  20                  25  
 Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys Ser Ser  
                   30                  35                  40  
 Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg Asn Arg  
                   45                  50                  55  
 Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn  
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 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe  
           -25                  -20                  -15  
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Ile Ile  
           -10                  -5                  1                  5  
 Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser  
                   10                  15                  20  
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys  
                   25                  30                  35  
 Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met  
           40                  45                  50  
 Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Gly Val  
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<210> 124  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens  
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 <222> -15...-1  
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 Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu  
           5                  10                  15  
 Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp  
           20                  25                  30  
 Met Leu Val

<210> 125  
 <211> 56  
 <212> PRT  
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 Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg  
           -10                          -5                          1                          5  
 Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala  
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 Trp Cys Ile Gln Pro Trp Ala Lys  
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<210> 126  
 <211> 162  
 <212> PRT  
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 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln  
           -5                          1                          5                          10  
 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala  
                           15                          20                          25  
 Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser  
           30                          35                          40  
 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly  
           45                          50                          55  
 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His  
           60                          65                          70                          75  
 Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp  
                           80                          85                          90  
 Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val  
           95                          100                          105  
 Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro  
           110                          115                          120  
 His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val  
           125                          130                          135  
 Arg Arg  
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<210> 127  
 <211> 126  
 <212> PRT  
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 <222> -68...-1  
 <400> 127



Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe  
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 Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu  
                   -50                  -45                  -40  
 His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu  
                   -35                  -30                  -25  
 Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu  
                   -20                  -15                  -10                  -5  
 Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg  
                   1                  5                  10  
 Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly  
                   15                  20                  25  
 Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe  
                   30                  35                  40  
 Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala  
 45                  50                  55

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 <211> 140  
 <212> PRT  
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 Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser  
                   -20                  -15                  -10  
 Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu His  
                   -5                  1                  5  
 Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val  
                   10                  15                  20  
 Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro  
 25                  30                  35                  40  
 Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu  
                   45                  50                  55  
 Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr  
                   60                  65                  70  
 Leu Ala Phe Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu  
                   75                  80                  85  
 Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn  
                   90                  95                  100

<210> 129  
 <211> 43  
 <212> PRT  
 <213> Homo sapiens  
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 <222> -24...-1  
 <400> 129

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 Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser  
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 Pro Tyr Phe Lys Met His Lys Pro Val Thr Met  
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 <211> 69  
 <212> PRT  
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       -5                      1                      5                      10  
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr  
               15                      20                      25  
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala  
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 Val Leu Cys Gln Lys  
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<210> 131  
 <211> 78  
 <212> PRT  
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 <400> 131  
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 Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val  
               1                      5                      10  
 Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr  
       15                      20                      25  
 Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val  
 30                      35                      40                      45  
 Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala  
                       50                      55

<210> 132  
 <211> 80  
 <212> PRT  
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 <400> 132  
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 Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser  
       -30                      -25                      -20  
 Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe  
       -15                      -10                      -5                      1  
 Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro  
               5                      10                      15  
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[illegible]

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<211> 1053
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 131..169
<223> Von Heijne matrix
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      seq MLAVSLTVPLIGA/MM
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<221> polyA_site  
<222> 1042..1053  
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gaccttcttg	atg	ctg	gct	gtt	tct	ctc	acc	gtt	ccc	ctg	ctt	gga	gcc	169		
	Met	Leu	Ala	Val	Ser	Leu	Thr	Val	Pro	Leu	Leu	Gly	Ala			
				-10					-5							
atg	atg	ctg	ctg	gaa	tct	cct	ata	gat	cca	cag	cct	ctc	agc	ttc	aaa	217
Met	Met	Leu	Leu	Glu	Ser	Pro	Ile	Asp	Pro	Gln	Pro	Leu	Ser	Phe	Lys	
1			5					10				15				
gaa	ccc	ccg	ctc	ttg	ctt	ggg	gtt	ctg	cat	cca	aat	acg	aag	ctg	cga	265
Glu	Pro	Pro	Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	
			20					25				30				
cag	gca	gaa	agg	ctg	ttt	gaa	aat	caa	ctt	gtt	gga	ccg	gag	tcc	ata	313
Gln	Ala	Glu	Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	
		35					40				45					
gca	cat	att	ggg	gat	gtg	atg	ttt	act	ggg	aca	gca	gat	ggc	cgg	gtc	361
Ala	His	Ile	Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	
	50					55					60					
gta	aaa	ctt	gaa	aat	ggg	gaa	ata	gag	acc	att	gcc	cgg	ttt	ggg	tcg	409
Val	Lys	Leu	Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser	
65					70				75					80		
ggc	cct	tcg	aaa	acc	cga	ggg	gat	gag	cct	gtg	tgt	ggg	aga	ccc	ctg	457
Gly	Pro	Cys	Lys	Thr	Arg	Gly	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	
			85					90				95				
ggg	atc	cgt	gca	ggg	ccc	aat	ggg	act	ctc	ttt	gtg	gcc	gat	gca	tac	505
Gly	Ile	Arg	Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr	
			100					105				110				
aaq	gga	cta	ttt	gaa	gta	aat	ccc	tqq	aaa	cgt	gaa	gtg	aaa	ctg	ctg	553

[illegible]

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 tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatggtttat 306  
 Tyr Val Cys Val Phe Ile  
 55  
 ttctattttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca 366  
 tattttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga 426  
 tattttctcta gttttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg 486  
 cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt 546  
 cagagaagaa catttaaagg gttaatatatt ttgaaacggt ttcagataat atctatttga 606  
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 <210> 136  
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 <223> Von Heijne matrix  
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 seq GVLLEPFVHQVGG/HS  
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 <221> polyA\_signal  
 <222> 1080..1085  
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 <221> polyA\_site  
 <222> 1101..1112  
 <400> 136  
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 ccgctgggact ccgctgcctc ccccatctcc ccgccatctg cgcccggagg atg agc 116  
 Met Ser  
 cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 164  
 Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu  
 -25 -20 -15  
 ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 212  
 Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg  
 -10 -5 1 5  
 ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag 260  
 Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln  
 10 15 20  
 ttc tac gag acc ctc cct gct gag atg cgc aaa ttc tct ccc cag tac 308  
 Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro Gln Tyr  
 25 30 35  
 aaa gga caa agc caa agg ccc ctt gtt agc tgg cca tcc ctg ccc cat 356  
 Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu Pro His  
 40 45 50  
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 Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val Ala  
 55 60 65  
 tgaatacccc accccggctc ctctgcaccc agagctgggg gccacctcag aagtgtcatc 461  
 tctctctgag cacgcattcc cctgcagcag tcgaggactg agcagattga gtgatgctgg 521  
 ggcagagagg cctgagagga aagggtgttca gccagtcggt tgtaaggcgc tcgtcggcac 581  
 ctgctgaaac gccccacct gacagcccca tcctcaaaga ctgtcttaat tactcatggc 641  
 aggttctaga gacttaaggg gaaaagctgc tttcaaggcc accacatgtc tgtgctcccc 701  
 aaccagctct atctgccttg tgttcatttt gttattttgt gacgtgagac agcaaagacc 761  
 aataaaaaca tattttataa gaacaaaagg cctgggtgcc taccctgtgt ggggcactgt 821

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gcttttgctta	cccagtcctc	ccttactcct	ggatgcttct	taaccctcag	gcaaacctgt	941
gttccccctg	tattcaggct	ctgctttaaa	gcaagccatg	aggctgttgg	agttttctgtt	1001
tagggcatta	aaaattcccc	caaactataa	agagcaatgt	tttcagtcct	ttaggattag	1061
aagaattaca	taaaaattaa	taaacatttt	caatgatgga	aaaaaaaaaa	a	1112

<210> 137

<211> 547

<212> DNA

<213> Homo sapiens

<220>

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<222> 359..454

<223> Von Heijne matrix

score 4

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<222> 536..547

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ggttttattg	tgagctggcc	ttggaattaa	accaccacca	acacactttt	ggattatcag	180
aagggtggaag	gagtgcacaaa	atgtcattcc	catgcttgtc	tgccaggcaa	cctgggtgtcc	240
attctttatg	acgcctttcc	tgaatcacag	gtgcattggg	gtgcttcctc	ctccccagga	300
ctccccacca	actttgtgaa	cacaaccac	ttagaggagt	tatctcagca	cattatga	358
atg ttg ggg acc acg ggc ctc ggg aca cag ggt cct tcc cag cag gct						406
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala						
-30	-25	-20				
ctg ggc ttt ttc tcc ttt atg tta ctt gga atg ggc ggg tgc ctg cct						454
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro						
-15	-10	-5				
gga ttc ctg cta cag cct ccc aat cga tct cct act ttg cct gca tcc						502
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser						
1	5	10	15			
acc ttt gcc cat taaagtcaat tctccaccca taaaaaaaaa aaa						547
Thr Phe Ala His						
20						

<210> 138

<211> 1198

<212> DNA

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 26..316

<223> Von Heijne matrix

score 4

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<220>

<221> polyA\_signal

<222> 1164..1169

<220>

<221> polyA\_site

<222> 1187..1198

<400> 138

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Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser
                                -85                                -80                                -75
gat aga gat gga gta cct gtt gtt aaa gtg gca aat gac aat gct cca      148
Asp Arg Asp Gly Val Pro Val Val Lys Val Ala Asn Asp Asn Ala Pro
                                -70                                -65                                -60
gag cat gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca      196
Glu His Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr
                                -55                                -50                                -45
gac caa gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt      244
Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys
-40                                -35                                -30                                -25
tac tat aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg      292
Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val
                                -20                                -15                                -10
gtg agt ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc      340
Val Ser Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser
                                -5                                1                                5
cta gaa aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg      388
Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val
                                10                                15                                20
gaa gtt tct taatctgaca gtggtttcag tgtgtacctt atcttcatta      437
Glu Val Ser
25
taacaacaca atatcaatcc agcaatcttt agactacaat aatgctttta tccatgtgct      497
caagaaaggg cccctttttc caacttatac taaagagcta gcatatagat gtaatttata      557
gatagatcag ttgtctatatt ttctggtgta gggcttttct tatttagtga gatctaggga      617
taccacagaa atggttcagt ctatcacagc tcccatggag ttagtctggt caccagatat      677
ggatgagaga ttctattcag tggattagaa tcaaactggt acattgatcc acttgagccg      737
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ctgctcttta atgaaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg      1037
taaccaatca gtgttttaaat gtttgtgtgt tcttcataaa atttaaatac aattcgttat      1097
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Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly Ala
1 5 10
agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa tgt    197
Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu Cys
15 20 25 30
gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc ctt    245
Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu
35 40 45
ctg ggc ctg ccc gct gac atc cag gct gcc cag gcc atg atg gtg aca    293
Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr
50 55 60
tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc atg    341
Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met
65 70 75
aga tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg gcg    389
Arg Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala
80 85 90
gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc att    437
Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile
95 100 105 110
cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca cca    485
Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
115 120 125
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Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr Leu
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ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc tgc    581
Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu Cys
145 150 155
ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc tac    629
Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala Tyr
160 165 170
caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa cct    677
Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln Pro
175 180 185 190
ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat gtg    725
Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr Val
195 200 205
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Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu
-25                -20                -15                -10
ttg ctg att gct gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc      151
Leu Leu Ile Ala Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile
                -5                1                5
cga tat gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa      199
Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys
        10                15                20
ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag gga agt atc      247
Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Gly Ser Ile
        25                30                35
tgt tgaagggcta ctatctttcc ttggcccttc tcccttggtg ggactcaatc      300
Cys
40
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caaagactcc aagtttgatg actggaagaa tattcgagga cccaggcctt gggaagatcc      420
tgacctcctc caaggaagaa atccagaaag ccttaagact aagacaactt gactctgctg      480
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tgcttttagta gtagttaaaa gtagtaactg ctactgtatt tagtggggtg gaattcagaa      120
gaaatttgaa gaccagatca tgggtggtct gcatgtgaat gaacagga atg agc cag      177

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Thr	Ala	Trp	Leu	Ser	Leu	Leu	Ser	Ser	Ser	Pro	Phe	Gly	Pro	Phe	Ser			
				-25				-20				-15						
gcc	ctt	aca	ttt	ttg	ttt	ctc	cat	cta	cca	cca	tcc	acc	agt	cta	ttt	273		
Ala	Leu	Thr	Phe	Leu	Phe	Leu	His	Leu	Pro	Pro	Ser	Thr	Ser	Leu	Phe			
				-10				-5				1						
att	aac	tta	gca	aga	gga	caa	ata	aag	ggc	cct	ctt	ggc	ttg	att	ttg	321		
Ile	Asn	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Gly	Pro	Leu	Gly	Leu	Ile	Leu			
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ctt	ctt	tct	ttc	tgt	gga	gga	tat	act	aag	tgc	gac	ttt	gcc	cta	tcc	369		
Leu	Leu	Ser	Phe	Cys	Gly	Gly	Tyr	Thr	Lys	Cys	Asp	Phe	Ala	Leu	Ser			
				20				25				30						
tat	ttg	gaa	atc	cct	aac	aga	att	gag	ttt	tct	att	atg	gat	cca	aaa	417		
Tyr	Leu	Glu	Ile	Pro	Asn	Arg	Ile	Glu	Phe	Ser	Ile	Met	Asp	Pro	Lys			
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aga	aaa	aca	aaa	tgc	taatgaagcc	atcagtc	caag	ggtcacatgc	caataa	acaa	472							
Arg	Lys	Thr	Lys	Cys														
				55														
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						1167												

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Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp	
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Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu	
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Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys	
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Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro	
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Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr	
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Met Trp Trp	
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Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr	
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Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His	
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Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro	
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Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys	
35 40 45	
att gct acc att tat gtt cgt tat aag caa gtt cat gct ctg agt cct	356

Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala	Leu	Ser	Pro		
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Glu	Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly		
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Ile	Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Lys	Thr		
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acc	ctt	ttt	gct	gca	cat	gta	agt	gga	gct	gtg	ctt	acc	ttt	ggt	atg	500	
Thr	Leu	Phe	Ala	Ala	His	Val	Ser	Gly	Ala	Val	Leu	Thr	Phe	Gly	Met		
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ggc	tca	tta	tat	atg	ttt	gtt	cag	acc	atc	ctt	tcc	tac	caa	atg	cag	548	
Gly	Ser	Leu	Tyr	Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln		
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Pro	Lys	Ile	His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val		
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Ile	Trp	Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val		
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Leu	His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp		
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Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr	Tyr	Ile		
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Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn	Asn	Glu	Arg	Thr		
			225				230				235						
cgg	cta	ctt	tcc	aga	gat	att	aga	tgaaaggata	aaatatttct	gtaatgatta						938	
Arg	Leu	Leu	Ser	Arg	Asp	Ile	Arg										
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aacagtccat gtgggtgatt cagctctg atg gga tgt gtt ttc cag agc aca      232
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gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag      280
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu
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cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg      328
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val
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cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac atc tta      376
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu
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Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln
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gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc      472
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe
   75           80           85
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa ggt acg      520
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Gly Thr
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Gln Met Leu Thr
105
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Cys Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln
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Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr
5 10 15
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Leu Lys Tyr His Trp Pro
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aagactccag tgggggtggc agtaggagag cacgttcaga gggaagagcc atctcaacag      661
aatcgacca aactatactt tcaggatgaa tttcttcttt ctgccatctt ttggaataaa      721
tattttcctc ctttctatgt aaaaaaaaaa aaa      754

<210> 146
<211> 1073
<212> DNA
<213> Homo sapiens
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<222> 98..181
<223> Von Heijne matrix
score 3.59999990463257
seq PLSDSWALLPASA/GV
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<221> polyA_signal
<222> 1035..1040
<220>
<221> polyA_site
<222> 1060..1073
<400> 146
ccgattacag ctaggtagtg gagcgccgct gcttacctgg gtgcaggaga cagccggagt      60
cgctgggggga gctccgcgcc gccggacgcc cgtgacc atg tgg agg ctg ctg gct      115
Met Trp Arg Leu Leu Ala
-25
cgc gct agt gcg ccg ctc ctg cgg gtg ccc ttg tca gat tcc tgg gca      163
Arg Ala Ser Ala Pro Leu Leu Arg Val Pro Leu Ser Asp Ser Trp Ala
-20 -15 -10
ctc ctc ccc gcc agt gct ggc gta aag aca ctg ctc cca gta cca agt      211
Leu Leu Pro Ala Ser Ala Gly Val Lys Thr Leu Leu Pro Val Pro Ser
-5 1 5 10
ttt gaa gat gtt tcc att cct gaa aaa ccc aag ctt aga ttt att gaa      259
Phe Glu Asp Val Ser Ile Pro Glu Lys Pro Lys Leu Arg Phe Ile Glu
15 20 25
agg gca cca ctt gtg cca aaa gta aga aga gaa cct aaa aat tta agt      307
Arg Ala Pro Leu Val Pro Lys Val Arg Arg Glu Pro Lys Asn Leu Ser
30 35 40
gac ata cgg gga cct tcc act gaa gct acg gag ttt aca gaa ggc aat      355
Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr Glu Phe Thr Glu Gly Asn
45 50 55

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ttt gca atc ttg gca ttg ggt ggt ggc tac ctg cat tgg ggc cac ttt	403
Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr Leu His Trp Gly His Phe	
60 65 70	
gaa atg atg cgc ctg aca atc aac cgc tct atg gac ccc aag aac atg	451
Glu Met Met Arg Leu Thr Ile Asn Arg Ser Met Asp Pro Lys Asn Met	
75 80 85 90	
ttt gcc ata tgg cga gta cca gcc cct ttc aag ccc atc act cgc aaa	499
Phe Ala Ile Trp Arg Val Pro Ala Pro Phe Lys Pro Ile Thr Arg Lys	
95 100 105	
agt gtt ggg cat cgc atg ggg gga ggc aaa ggt gct att gac cac tac	547
Ser Val Gly His Arg Met Gly Gly Lys Gly Ala Ile Asp His Tyr	
110 115 120	
gtg aca cct gtg aag gct ggc cgc ctt gtt gta gag atg ggt ggg cgt	595
Val Thr Pro Val Lys Ala Gly Arg Leu Val Val Glu Met Gly Gly Arg	
125 130 135	
tgt gaa ttt gaa gaa gtg caa ggt ttc ctt gac cag gtt gcc cac aag	643
Cys Glu Phe Glu Glu Val Gln Gly Phe Leu Asp Gln Val Ala His Lys	
140 145 150	
ttg ccc ttc gca gca aag gct gtg agc cgc ggg act cta gag aag atg	691
Leu Pro Phe Ala Ala Lys Ala Val Ser Arg Gly Thr Leu Glu Lys Met	
155 160 165 170	
cga aaa gat caa gag gaa aga gaa cgt aac aac cag aac ccc tgg aca	739
Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn Asn Gln Asn Pro Trp Thr	
175 180 185	
ttt gag cga ata gcc act gcc aac atg ctg ggc ata cgg aaa gta ctg	787
Phe Glu Arg Ile Ala Thr Ala Asn Met Leu Gly Ile Arg Lys Val Leu	
190 195 200	
agc cca tat gac ttg acc cac aag ggg aaa tac tgg ggc aag ttc tac	835
Ser Pro Tyr Asp Leu Thr His Lys Gly Lys Tyr Trp Gly Lys Phe Tyr	
205 210 215	
atg ccc aaa cgt gtg tagtgagtgt aggagataac tgtatatagg ctactgaaag	890
Met Pro Lys Arg Val	
220	
aaggattctg catttctatt cccctcagcc taccactga agtctttggg tagctcttaa	950
gccataacta aggagcagca tttgagtaga tttctgaaaa acgatgttat ttgttgattt	1010
aaaaagaaaa ctgtattttt attaaataaa atttaaacat cacttcagga aaaaaaaaaa	1070
aaa	1073

<210> 147

<211> 413

<212> DNA

<213> Homo sapiens

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<221> sig\_peptide

<222> 46..189

<223> Von Heijne matrix

score 4.09999990463257

seq VFMLIVSVLALIP/ET

<220>

<221> polyA\_signal

<222> 377..382

<220>

<221> polyA\_site

<222> 402..413

<400> 147

tgagaagagt tgagggaaag tgctgctgct gggctctgcag acgcg atg gat aac gtg  
Met Asp Asn Val

57

-45

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cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac      105
Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly His
      -40      -35      -30
gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta aca aca gta      153
Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val
      -25      -20      -15
ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca      201
Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
      -10      -5      1
ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgc      249
Leu Thr Val Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys
5      10      15      20
ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc      297
Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser
      25      30      35
ggg cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg      342
Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
      40      45      50
taattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca      402
aaaaaaaaa a      413

<210> 148
<211> 609
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      seq TCCHLGLPHPVRA/PR
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<222> 579..584
<220>
<221> polyA_site
<222> 598..609
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tgtcggaggtt ggaaagggac gcctgggtttc cccccaagcg aaccgggatg ggaagtgact      60
tcaatgagat tgaacttcag ctggattgaa agagaggcta gaagttccgc ttgccagcag      120
cctccttagt agagcgga atg agt aat acc cac acg gtg ctt gtc tca ctt      171
      Met Ser Asn Thr His Thr Val Leu Val Ser Leu
      -30      -25
ccc cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac      219
Pro His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His
-20      -15      -10      -5
ccg gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct      267
Pro Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro
      1      5      10
agg tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc      315
Arg Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe
      15      20      25
cta aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg      363
Leu Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser
      30      35      40
gct gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta      411
Ala Asp Arg Cys Asp Leu
45      50

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ttttatcctt gacttggtac aagttttggg atttctgaaa agaccataca gataaccaca	471
aatatcaaga aagtcgtctt cagtattaag tagaatttag atttaggttt ccttcctgct	531
ccccacctcc ttcgaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg	591
agctgcaaaaa aaaaaaaaa	609

<210> 149  
 <211> 522  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> polyA\_site  
 <222> 512..522  
 <220>  
 <221> misc\_feature  
 <222> 11  
 <223> n=a, g, c or t

<400> 149	
ccaactgcag nttcgaat accgagcgga gaggagatgc acacggcact cgagtgtgag	60
gaaaaataga a atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt	110
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys	
1 5 10	
ttg ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat	158
Leu Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His	
15 20 25	
gac cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa	206
Asp His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu	
30 35 40 45	
ttg gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa	254
Leu Glu Pro Ser Lys Phe Ser Lys Gln Ala Glu Asn Glu Lys Lys	
50 55 60	
tac tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta	302
Tyr Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu	
65 70 75	
tcc ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag	350
Ser Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu	
80 85 90	
aga aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt	398
Arg Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val	
95 100 105	
tct cat tta ggt att ttg gca gtt caa gag gga aag cat ttt cac tca	446
Ser His Leu Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser	
110 115 120 125	
cat aac cac cag cat tcc cat aat cat tta aat tca gaa aat caa act	494
His Asn His Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr	
130 135 140	
gtg acc agt gta tcc aca aaaaaaaaa	522
Val Thr Ser Val Ser Thr	
145	

<210> 150  
 <211> 1322  
 <212> DNA  
 <213> Homo sapiens  
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 <221> sig\_peptide  
 <222> 126..260  
 <223> Von Heijne matrix  
 score 4.59999990463257

seq VLVYLVTAERVWS/DD

<220>

<221> polyA\_signal

<222> 1283..1288

<220>

<221> polyA\_site

<222> 1309..1322

<400> 150

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gctgctggga gccaggagag ccctgaggag tagtcactca gtagcagctg acgcgtgggt      120
ccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc aac aag      170
    Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys
      -45                -40                -35
tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc atc ttc      218
Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe
      -30                -25                -20                -15
cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt gat gac      266
Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp
                  -10                -5                1
cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc aac gtc      314
His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val
                  5                10                15
tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg gcc ctg      362
Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu
                  20                25                30
cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg cac gtg      410
Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val
                  35                40                45                50
gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat ggg gag      458
Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu
                  55                60                65
aac agt ggg cgc ctc tac ctg aac ccc ggc aag aag cgg ggt ggg ctc      506
Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu
                  70                75                80
tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg gac atc      554
Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile
                  85                90                95
gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc ctc cct      602
Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro
                  100                105                110
cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg gac tgc      650
Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys
                  115                120                125                130
ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc atg gtg      698
Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val
                  135                140                145
gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc atc tac      746
Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr
                  150                155                160
ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa gct caa      794
Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln
                  165                170                175
gcc atg tgc aca ggt cat cac ccc cac gat acc acc tct tcc tgc aaa      842
Ala Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys
                  180                185                190
caa gac gac ctc ctt tcg ggt gac ctc atc ttt ctg ggc tca gac agt      890
Gln Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser
                  195                200                205                210

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cat cct cct ctc tta cca gac cgc ccc cga gac cat gtg aag aaa acc      938
His Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr
                215                220                225
atc ttg tgaggggctg cctggactgg tctggcaggt tgggcctgga tggggaggct      994
Ile Leu
ctagcatctc tcataggtgc aacctgagag tgggggagct aagccatgag gtaggggcag      1054
gcaagagaga ggattcagac gctctgggag ccagttccta gtcctcaact ccagccacct      1114
gccccagctc gacggcactg ggccagtcc cctctgctc tgcagctcgg tttccttttc      1174
tagaatggaa atagtgaggg ccaatgccc gggttggagg gaggagggcg ttcatagaag      1234
aacacacatg cgggcacctt catcgtgtgt ggcccactgt cagaacttaa taaaagtcaa      1294
ctcatttgct gggtaaaaaa aaaaaaaa      1322

<210> 151
<211> 1290
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 50..160
<223> Von Heijne matrix
      score 4
      seq PLSLDCGHSLCRA/CI
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<221> polyA_site
<222> 1280..1290
<400> 151
gaggagagcc tcaggagtta ggaccagaag aagccagga agcagtgca atg gct tca      58
                               Met Ala Ser
                               -35
aaa atc ttg ctt aac gta caa gag gag gtg acc tgt ccc atc tgc ctg      106
Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile Cys Leu
      -30                -25                -20
gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc ctc tgc      154
Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser Leu Cys
      -15                -10                -5
cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc atg gga      202
Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser Met Gly
      1                5                10
gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt gaa cat      250
Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser Phe Glu His
      15                20                25                30
cta cag gct aat cag cat ctg gcc aac ata gtg gag aga ctc aag gag      298
Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg Leu Lys Glu
      35                40                45
gtc aag ttg agc cca gac aat ggg aag aag aga gat ctc tgt gat cat      346
Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu Cys Asp His
      50                55                60
cat gga gag aaa ctc cta ctc ttc tgt aag gag gat agg aaa gtc att      394
His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg Lys Val Ile
      65                70                75
tgc tgg ctt tgt gag cgg tct cag gag cac cgt ggt cac cac aca gtc      442
Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His His Thr Val
      80                85                90
ctc acg gag gaa gta ttc aag gaa tgt cag gag aaa ctc cag gca gtc      490
Leu Thr Glu Glu Val Phe Lys Glu Cys Gln Glu Lys Leu Gln Ala Val
      95                100                105                110
ctc aag agg ctg aag aag gaa gag gag gaa gct gag aag ctg gaa gct      538
Leu Lys Arg Leu Lys Lys Glu Glu Glu Glu Ala Glu Lys Leu Glu Ala

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	115	120	125	
	gac atc aga gaa gag aaa act tcc tgg aag tat cag gta caa act gag			586
	Asp Ile Arg Glu Glu Lys Thr Ser Trp Lys Tyr Gln Val Gln Thr Glu			
	130	135	140	
	aga caa agg ata caa aca gaa ttt gat cag ctt aga agc atc cta aat			634
	Arg Gln Arg Ile Gln Thr Glu Phe Asp Gln Leu Arg Ser Ile Leu Asn			
	145	150	155	
	aat gag gag cag aga gag ctg caa aga ttg gaa gaa gaa gaa aag aag			682
	Asn Glu Glu Gln Arg Glu Leu Gln Arg Leu Glu Glu Glu Glu Lys Lys			
	160	165	170	
	acg ctg gat aag ttt gca gag gct gag gat gag cta gtt cag cag aag			730
	Thr Leu Asp Lys Phe Ala Glu Ala Glu Asp Glu Leu Val Gln Gln Lys			
	175	180	185	190
	cag ttg gtg aga gag ctc atc tca gat gtg gag tgt cgg agt cag ttg			778
	Gln Leu Val Arg Glu Leu Ile Ser Asp Val Glu Cys Arg Ser Gln Trp			
	195	200	205	
	tca aca atg gag ctg ctg cag gac atg agt gga atc atg aaa tgg agt			826
	Ser Thr Met Glu Leu Leu Gln Asp Met Ser Gly Ile Met Lys Trp Ser			
	210	215	220	
	gag atc tgg agg ctg aaa aag cca aaa atg gtt tcc aag aaa ctg aag			874
	Glu Ile Trp Arg Leu Lys Lys Pro Lys Met Val Ser Lys Lys Leu Lys			
	225	230	235	
	act gta ttc cat gct cca gat ctg agt agg atg ctg caa atg ttt aga			922
	Thr Val Phe His Ala Pro Asp Leu Ser Arg Met Leu Gln Met Phe Arg			
	240	245	250	
	gaa ctg aca gct gtc cgg tgc tac tgg gtg gat gtc aca ctg aat tca			970
	Glu Leu Thr Ala Val Arg Cys Tyr Trp Val Asp Val Thr Leu Asn Ser			
	255	260	265	270
	gtc aac cta aat ttg aat ctt gtc ctt tca gaa gat cag aga caa gtg			1018
	Val Asn Leu Asn Leu Asn Leu Val Leu Ser Glu Asp Gln Arg Gln Val			
	275	280	285	
	ata tct gtg cca att tgg cct ttt cag tgt tat aat tat ggt gtc ttg			1066
	Ile Ser Val Pro Ile Trp Pro Phe Gln Cys Tyr Asn Tyr Gly Val Leu			
	290	295	300	
	gga tcc caa tat ttc tcc tct ggg aaa cat tac tgg gaa gtg gac gtg			1114
	Gly Ser Gln Tyr Phe Ser Ser Gly Lys His Tyr Trp Glu Val Asp Val			
	305	310	315	
	tcc aag aaa act gcc tgg atc ctg ggg gta tac tgt aga aca tat tcc			1162
	Ser Lys Lys Thr Ala Trp Ile Leu Gly Val Tyr Cys Arg Thr Tyr Ser			
	320	325	330	
	cgc cat atg aag tat gtt gtt aga aga tgt gca aat cgt caa aat ctt			1210
	Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg Gln Asn Leu			
	335	340	345	350
	tac acc aaa tac aga cct cta ttt ggc tac tgg gtt ata ggg tta cag			1258
	Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile Gly Leu Gln			
	355	360	365	
	aat aaa tgt aag tat ggt gcc aaaaaaaaaa a			1290
	Asn Lys Cys Lys Tyr Gly Ala			
	370			

<210> 152

<211> 1364

<212> DNA

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 83..139

<223> Von Heijne matrix

score 8.60000038146973

seq LLWLALACSPVHT/TL

<220>

<221> polyA\_site

<222> 1356..1354

<400> 152

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gcctgggagc tgaggcagcc accgtctcag cctggccagc cctctggacc ccgaggttgg      60
accctactgt gacacaccta cc atg cgg aca ctc ttc aac ctc ctc tgg ctt      112
                               Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
                               -15                               -10
gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc      160
Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala
                               -5                               1                               5
aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat      208
Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp
                               10                               15                               20
aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag      256
Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu
                               25                               30                               35
agt gtg gtt ctt gag cat cgc agc tac tgc tgc gca aag gcc cgg gac      304
Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp
                               40                               45                               50                               55
aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc      352
Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser
                               60                               65                               70
cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc      400
His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile
                               75                               80                               85
tca ccc gtc tgg ctg cag ttg aag aga cgt ggc cgt gag atg ttt gag      448
Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu
                               90                               95                               100
gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg      496
Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg
                               105                               110                               115
aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac      544
Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp
                               120                               125                               130                               135
tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata      592
Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile
                               140                               145                               150
gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc      640
Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe
                               155                               160                               165
gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc      688
Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg
                               170                               175                               180
gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gcc ctg cac cag      736
Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln
                               185                               190                               195
gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg      784
Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly
                               200                               205                               210                               215
acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc      832
Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala
                               220                               225                               230
ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg      880
Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala
                               235                               240                               245

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cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc	928
His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val	
250 255 260	
cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg	976
Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly	
265 270 275	
ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag	1024
Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu	
280 285 290 295	
cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc	1072
Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro	
300 305 310	
cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag	1120
Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys	
315 320 325	
aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc	1168
Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser	
330 335 340	
ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct	1216
Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser	
345 350 355	
atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac gac ctg ctc	1261
Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu	
360 365 370	
taggtgggca ttgcggcctc cgcggtggac gtgttctttt ctaagccatg gagtgagtga	1321
gcaggtgtga aatacaggcc tccactccgt ttgcaaaaaa aaa	1364

<210> 153

<211> 1470

<212> DNA

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 57..95

<223> Von Heijne matrix  
score 3.90000009536743  
seq MLLSIGMLMLSAT/QV

<220>

<221> polyA\_signal

<222> 1438..1443

<220>

<221> polyA\_site

<222> 1458..1470

<400> 153

gctggcaaga ctgtttgtgt tgcgggggcc ggacttcaag gtgattttac aacgag atg	59
Met	
ctg ctc tcc ata ggg atg ctc atg ctg tca gcc aca caa gtc tac acc	107
Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr	
-10 -5 1	
gtc ttg act gtc cag ctc ttt gca ttc tta aac cca ctg cct gta gaa	155
Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val Glu	
5 10 15 20	
gca gac att tta gca tat aac ttt gaa aat gca tct cag aca ttt gat	203
Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp	
25 30 35	
gac ctc cct gca aga ttt ggt tat aga ctt cca gct gaa ggt tta aag	251
Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu Lys	
40 45 50	

ggt ttt tta att aac tca aaa cca gag aat gcc tgt gaa ccc ata gtg	299
Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile Val	
55 60 65	
cct cca cca gta aaa gac aat tca tct ggc act ttc atc gtg tta att	347
Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu Ile	
70 75 80	
aga aga ctt gat tgt aat ttt gat ata aag gtt tta aat gca cag aga	395
Arg Arg Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln Arg	
85 90 95 100	
gca gga tac aag gca gcc ata gtt cac aat gtt gat tct gat gac ctc	443
Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp Leu	
105 110 115	
att agc atg gga tcc aac gac att gag gta cta aag aaa att gac att	491
Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp Ile	
120 125 130	
cca tct gtc ttt att ggt gaa tca tca gct agt tct ctg aaa gat gaa	539
Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp Glu	
135 140 145	
ttc aca tat gaa aaa ggg ggc cac ctt atc tta gtt cca gaa ttt agt	587
Phe Thr Tyr Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe Ser	
150 155 160	
ctt cct ttg gaa tac tac cta att ccc ttc ctt atc ata gtg ggc atc	635
Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Ile Val Gly Ile	
165 170 175 180	
tgt ctc atc ttg ata gtc att ttc atg atc aca aaa ttt gtc cag gat	683
Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Phe Val Gln Asp	
185 190 195	
aga cat aga gct aga aga aac aga ctt cgt aaa gat caa ctt aag aaa	731
Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys Lys	
200 205 210	
ctt cct gta cat aaa ttc aag aaa gga gat gag tat gat gta tgt gcc	779
Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys Ala	
215 220 225	
att tgt ttg gat gag tat gaa gat gga gac aaa ctc aga atc ctt ccc	827
Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu Pro	
230 235 240	
tgt tcc cat gct tat cat tgc aag tgt gta gac cct tgg cta act aaa	875
Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr Lys	
245 250 255 260	
acc aaa aaa acc tgt cca gtg tgc agg caa aaa gtt gtt cct tct caa	923
Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser Gln	
265 270 275	
ggc gat tca gac tct gac aca gac agt agt caa gaa gaa aat gaa gtg	971
Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu Val	
280 285 290	
aca gaa cat acc cct tta ctg aga cct tta gct tct gtc agt gcc cag	1019
Thr Glu His Thr Pro Leu Leu Arg Pro Leu Ala Ser Val Ser Ala Gln	
295 300 305	
tca ttt ggg gct tta tcg gaa tcc cgc tca cat cag aac atg aca gaa	1067
Ser Phe Gly Ala Leu Ser Glu Ser Arg Ser His Gln Asn Met Thr Glu	
310 315 320	
tct tca gac tat gag gaa gac gac aat gaa gat act gac agt agt gat	1115
Ser Ser Asp Tyr Glu Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp	
325 330 335 340	
gca gaa aat gaa att aat gaa cat gat gtc gtg gtc cag ttg cag cct	1163
Ala Glu Asn Glu Ile Asn Glu His Asp Val Val Val Gln Leu Gln Pro	
345 350 355	
aat ggt gaa cgg gat tac aac ata gca aat act gtt tgactttcag	1209

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Asn Gly Glu Arg Asp Tyr Asn Ile Ala Asn Thr Val
      360                      365
aagatgattg gtttatttcc ctttaaaatg attaggtata tactgtaatt tgattttttg 1269
ctcccttaaa agatttctgt agaaataact tatttttttag tactctacag tttaatcaaa 1329
ttactgaaac aggacttttg atctggtatt tatctgccaa gaatatactt cattcactaa 1389
taatagactg gtgctgtaac tcaagcatca attcagctct tcttttggaa tgaaagtata 1449
gccaaaacaa aaaaaaaaaa a 1470

<210> 154
<211> 982
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 72..197
<223> Von Heijne matrix
      score 7.19999980926514
      seq ILFSLSFLLVIT/FP
<220>
<221> polyA_site
<222> 970..982
<400> 154
gctgcctgtt cttcacactt agtcctaaac ccatgaaaaa ttgccaagta taaaagcttc 60
tcaagaatga g atg gat tct agg gtg tct tca cct gag aag caa gat aaa 110
      Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys
      -40                      -35                      -30
gag aat ttc gtg ggt gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg 158
Glu Asn Phe Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp
      -25                      -20                      -15
atc ctg ttt tcc ctc tct ttc ctg ttg gtg atc att acc ttc ccc atc 206
Ile Leu Phe Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile
      -10                      -5                      1
tcc ata tgg atg tgc ttg aag atc att agg gag tat gaa cgt gct gtt 254
Ser Ile Trp Met Cys Leu Lys Ile Ile Arg Glu Tyr Glu Arg Ala Val
      5                      10                      15
gta ttc cgt ctg gga cgc atc caa gct gac aaa gcc aag ggg cca ggt 302
Val Phe Arg Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly
      20                      25                      30                      35
ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aag gtt gac ctc 350
Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu
      40                      45                      50
cga aca gtt act tgc aac att cct cca caa gag atc ctc acc aga gac 398
Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp
      55                      60                      65
tcc gta act act cag gta gat gga gtt gtc tat tac aga atc tat agt 446
Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser
      70                      75                      80
gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa gca aca ttt 494
Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln Ala Thr Phe
      85                      90                      95
ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca cag acc ttg 542
Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu
      100                      105                      110                      115
tcc cag atc tta gct gga cga gaa gag atc gcc cat agc atc cag act 590
Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr
      120                      125                      130
tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg 638
Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val

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																686
																734
																782
																830
																878
																926
																982

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<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 90..278
<223> Von Heijne matrix
      score 3.5
      seq GLVCAGLADMARP/AE
<220>
<221> polyA_signal
<222> 704..709
<220>
<221> polyA_site
<222> 724..738
<400> 156
gggaaaagtg actagctccc ctctgttgtc agccagggac gagaacacag ccacgtctccc      60
accgggctgc caacgatccc tcggcggcgc atg tcg gcc gcc ggt gcc cga ggc      113
                               Met Ser Ala Ala Gly Ala Arg Gly
                               -60
ctg cgg gcc acc tac cac cgg ctc ccc gat aaa gtg gag ctg atg ctg      161
Leu Arg Ala Thr Tyr His Arg Leu Pro Asp Lys Val Glu Leu Met Leu
-55                               -50                               -45                               -40
ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc aga aca      209
Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro Arg Thr
                               -35                               -30                               -25
gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt gct gga      257
Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys Ala Gly
                               -20                               -15                               -10
ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct caa tct      305
Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala Gln Ser
                               -5                               1                               5
gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca ctt gta      353
Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser Leu Val
10                               15                               20                               25
att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt gtg ggg      401
Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe Val Gly
                               30                               35                               40
gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac caa gaa      449
Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn Gln Glu
                               45                               50                               55
cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc tgaacaatct      500
Leu Lys Ala Lys Ala His Lys
60
agatgtggac aaaaccattg ggacctagtt tattattttgg ttattgataa agcaaagcta      560
actgtgtggt tagaaggcac tgtaactggt agctagttct tgattcaata gaaaaatgca      620
gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg gatattagta      680
acatttttct accattttgtc cgtaataaac catacttgct cgtaaaaaaaaa aaaaaaaaa      738

<210> 157
<211> 649
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 88..147
<223> Von Heijne matrix
      score 12.3999996185303
      seq ALLLGALLGTAWA/RR

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<220>
<221> polyA_signal
<222> 619..624
<220>
<221> polyA_site
<222> 637..649
<400> 157
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aggaggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg      114
                               Met Lys Gly Trp Gly Trp Leu Ala Leu
                               -20                               -15

ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat      162
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
   -10                               -5                               1                               5

ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa      210
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
               10               15               20

att gcc cag gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg      258
Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
               25               30               35

atc aat cca gat ggc agc cag tca gtg gtg gag gta act gtt act gtt      306
Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Val
               40               45               50

ccc cca aac aaa gta gct cac tct ggc ttt gga tgaaattcga ctgcttaaaa      359
Pro Pro Asn Lys Val Ala His Ser Gly Phe Gly
   55               60

aggaccttgg tctaatagaa atgaagaaaa cagactcaga aaaaagattt ggctctgtct      419
catttggaag aagctgcagg cttattcccc atgcacttgc ttcctggctg caaaccttaa      479
tactttgttt ctgctgtaga atttggttagc aaacaggagg tcctgatcag cacccttctc      539
cacatccaca tgactgggttt ttaatgtagc actgtggtat acatgcaaac atccgttcaa      599
aatctgagtc ggagctaaaa ataaaaaatg aaaaaacaaa aaaaaaaaaa      649

<210> 158
<211> 714
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 33..92
<223> Von Heijne matrix
      score 12.3999996185303
      seq ALLLGALLGTAWA/RR
<220>
<221> polyA_site
<222> 703..714
<400> 158
agcagaggtg gagcgacccc attacgctaa ag atg aaa ggc tgg ggt tgg ctg      53
                               Met Lys Gly Trp Gly Trp Leu
                               -20                               -15

gcc ctg ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc      101
Ala Leu Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser
   -10                               -5                               1

cag gat ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa      149
Gln Asp Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu
   5               10               15

tgg gaa att gcc cag gtg gac ccc aag aag acc att cag atg gga tct      197
Trp Glu Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser
  20               25               30               35

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ttc cgg atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat	245
Phe Arg Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr	
40 45 50	
gcc cgc tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac	293
Ala Arg Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp	
55 60 65	
cgg atg aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag	341
Arg Met Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys	
70 75 80	
aac tac gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac	389
Asn Tyr Val Arg Val Val Arg Asn Gly Glu Ser Ser Glu Leu Asp	
85 90 95	
cta caa ggc atc cga atc gac tca gat att agc ggc acc ctc aag ttt	437
Leu Gln Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe	
100 105 110 115	
gcg tgt ggg agc att gtg gag gaa tac gag gat gaa ctc att gaa ttc	485
Ala Cys Gly Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe	
120 125 130	
ttt tcc cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga	533
Phe Ser Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg	
135 140 145	
aca gat ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta	578
Thr Asp Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu	
150 155 160	
tgaaccactg gagcagccca cactggcttg atggatcacc cccaggaggg gaaaatggtg	638
gcaatgcctt ttatatatta tggttttact gaaattaact gaaaaaatat gaaacaaaa	698
gtacaaaaaaa aaaaaa	714

<210> 159

<211> 596

<212> DNA

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 33..107

<223> Von Heijne matrix

score 5

seq MFAASLLAMCAGA/EV

<220>

<221> polyA\_signal

<222> 546..551

<220>

<221> polyA\_site

<222> 584..596

<400> 159

cacagttcct ctcctcctag agcctgccga cc atg ccc gcg ggc gtg ccc atg	53
Met Pro Ala Gly Val Pro Met	
-25 -20	
tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc gca	101
Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys Ala	
-15 -10 -5	
ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata cct	149
Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile Pro	
1 5 10	
gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga ctg	197
Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly Leu	
15 20 25 30	
aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt aaa	245

Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu Lys  
 35 40 45  
 taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc ttaatttatt 305  
 gcatcaaaact acttgtcctt aagcacttag tctaatagcta actgcaagag gaggtgctca 365  
 gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt tcttgaaaac 425  
 tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg tttagtcttg 485  
 aatataacgc gaaatagaat atttgaagt ctactatatg ggttgtcttt atttcatata 545  
 aattaagaaa ttattttaaa ctatgaacta gtttcattaa aaaaaaaga a 596  
  
 <210> 160  
 <211> 403  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> polyA\_signal  
 <222> 375..380  
 <220>  
 <221> polyA\_site  
 <222> 390..403  
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 agagcgcgag gactcggcgg ctgagcgcgc ccgacagcag ctagaggcgc tgctcaacaa 120  
 gact atg cgc att cgc atg aca gat gga cgg aca ctg gtc ggc tgc ttt 169  
 Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe  
 1 5 10 15  
 ctc tgc act gac cgt gac tgc aat gtc atc ctg ggc tcg gcg cag gag 217  
 Leu Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu  
 20 25 30  
 ttc ctc aag ccg tcg gat tcc ttc tct gcc ggg gag ccc cgt gtg ctg 265  
 Phe Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu  
 35 40 45  
 ggc ctg gcc atg gta ccc gga cac cac atc gtt tcc att gag gtg cag 313  
 Gly Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln  
 50 55 60  
 agg gag agt ctg acc ggg cct ccg tat ctc tgaccacgat ggcgcttacc 363  
 Arg Glu Ser Leu Thr Gly Pro Pro Tyr Leu  
 65 70  
 tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa 403  
  
 <210> 161  
 <211> 727  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> sig\_peptide  
 <222> 126..575  
 <223> Von Heijne matrix  
 score 8.60000038146973  
 seq LELLTSCSPASA/SQ  
 <220>  
 <221> polyA\_signal  
 <222> 670..675  
 <220>  
 <221> polyA\_site  
 <222> 721..727  
 <220>  
 <221> misc\_feature  
 <222> 257,376..377

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<223> n=a, g, c or t
<400> 161
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag      60
gacccgggggt aggggttttga gcccggtgga gctgccccac gcggcctcgt cctgccaacg    120
gtcgg atg gcg gag acg aag gac aca gcg cag atg ttg gtg acc ttc aag      170
    Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys
      -150                -145                -140
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
-135                -130                -125                -120
gcc cag agg acc ctg tac cga gag ggc atc ggg ttc ccn aaa cca gag      266
Ala Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu
      -115                -110                -105
ttg gtc cac ctg cta gag cat ggg cag gag ctg tgg ata gtg aag aga      314
Leu Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg
      -100                -95                -90
ggc ctc tca cat gct acc tgt gca gag ttt cac tct tgt tgc cca ggc      362
Gly Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly
      -85                -80                -75
tgg agt gca gtg gnn cgc cat ctc agc tca ctg caa ctt ctg cct ccc      410
Trp Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro
      -70                -65                -60
gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat tac      458
Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr
      -55                -50                -45                -40
agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta gag      506
Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu
      -35                -30                -25
acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc tca      554
Thr Gly Leu His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser
      -20                -15                -10
tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc gtg      602
Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val
      -5                1                5
agc cac cgt gcc cgg cag aga aaa act gct taaggttgaa aagagaaatt      652
Ser His Arg Ala Arg Gln Arg Lys Thr Ala
10                15
taagaaattg ctgacggaat aaaaacataa tagaactaca acaccgaagg aaatgaaaga      712
agcaaaaaaaaa aaaaaa      727

<210> 162
<211> 944
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<223> Von Heijne matrix
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      seq IILGCLALFLLLQ/RK
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<221> polyA_signal
<222> 913..918
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<222> 932..944
<400> 162
gaatcagggtt ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt      60

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tctgcttctg gaaggtgctg gacaaaaaac atg gaa cta att tcc cca aca gtg	113
Met Glu Leu Ile Ser Pro Thr Val	
-20 -15	
att ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag	161
Ile Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys	
-10 -5 1	
aat ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga	209
Asn Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly	
5 10 15	
gtt gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca	257
Val Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala	
20 25 30	
aga atc aag gta tgt ggt cgt ggc aga cgg ggt ctc cag agg aga caa	305
Arg Ile Lys Val Cys Gly Arg Gly Arg Arg Gly Leu Gln Arg Arg Gln	
35 40 45 50	
tgc ttt ctt ttt taaactttct ttcattgact cttaagtgcaggctagaac	357
Cys Phe Leu Phe	
acggggaaca tacctgcttg cctcaactaa aggatctagt catttctgaa ttcctctact	417
aacaattaac aacaatatcc tgtgcaaaat tttgcgaaag aaatgaaata caattgcagc	477
gtgcatcgac atttttggaa gtagagatta acttttctgta tttttacttc atcgaagtta	537
agttccaaat gtgtatgtgt taagtaaatg ttttcagtaa ttgggaaaga taaagtgtaa	597
tccaatttaa gtttgtgaaa atgagtaatt cgtatccaaa ttggagttaa caccaaagta	657
ttgtacaaat tgcttgacaca gttggtccgt acacaataga caggctctgt attttttagct	717
gacgttggtta tttgatgatg atgtactcca ttttactac ggcccgaaga gactagtaat	777
cctccttgta gtagatgttt ttgtcttgaa agtatctttt aaatgtctga gcactttaag	837
gaacagaccc ttattaatgt cttttaagtt ttattcaatt tccagtcaca aatattttat	897
ggtatttgat tgtctaataa atttgtatga tattaataaaaa aaaaaaa	944
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seq LETCGLLVSLVES/IW	
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gaccgggggt agggttttga gcccgtagga gctgccccac gcggcctcgt cctgccaacg	120
gtcgg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag	170
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys	
-50 -45 -40	
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg	218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu	
-35 -30 -25	
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt	266
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu	
-20 -15 -10	
ctg gtt tca cta gtg gaa agc att tgg ctg cat ata aca gaa aac cag	314
Leu Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln	

-5	1	5	
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag			362
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu			
10	15	20	25
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag			410
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln			
30	35	40	
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctgattg			470
tcctcaggct ggctcctcat agggatgctg ggtgctgcag ccttgactgg ggcagcaggc			530
ccccatgttc aatccatcct cccaccttgg aataaatgct ttcttttcac aatgagaaaa			590
aaaaaaaa			598

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 seq IILGCLALFLLLQ/RK

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 <222> 349..360  
 <400> 164

caggttccgt agccacagaa aagaagcaag ggacggcagg actgtttcac acttttctgc	60		
ttctggaagg tgctggacaa aaac atg gaa cta att tcc cca aca gtg att	111		
Met Glu Leu Ile Ser Pro Thr Val Ile			
-20	-15		
ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat	159		
Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn			
-10	-5	1	
ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt	207		
Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val			
5	10	15	
gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga	255		
Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg			
20	25	30	35
atc aag tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg	303		
Ile Lys Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met			
40	45	50	
acc ttt gtt act gaa gaa gaa gga att aat gtg ttt cta aaa tcc	348		
Thr Phe Val Thr Glu Glu Glu Gly Ile Asn Val Phe Leu Lys Ser			
55	60	65	
aaaaaaaa aa	360		

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 <212> DNA  
 <213> Homo sapiens  
 <220>  
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 <222> 77..124  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq SLFIYIFLTCSNT/SP  
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<221> polyA_signal
<222> 461..466
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<222> 477..490
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gaagcagtgt gtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca      112
                Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr
                -15                -10                -5
tgt agc aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt      160
Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly
                1                5                10
ctc ccc agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc      208
Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys
                15                20                25
tgc agg cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc      256
Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro
                30                35                40
ctc cac ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc      304
Leu His Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser
                45                50                55                60
tgg gac tgg gct gag gca ggg gct tgc ctc tat tct ccc taaccatact      353
Trp Asp Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
                65                70
gtcttccttt ccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct      413
cccttgccct ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa      473
gtgaaaaaaaa aaaaaaaa      490

<210> 166
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<222> 458..463
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<221> polyA_site
<222> 475..488
<400> 166
ccgcttccga aaagagacag acaatgcagc catcata atg aag gtg gac aaa gac      55
                Met Lys Val Asp Lys Asp
                1                5
cgg cag atg gtg gtg ctg gag gaa gaa ttt cgg aac att tcc cca gag      103
Arg Gln Met Val Val Leu Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu
                10                15                20
gag ctc aaa atg gag ttg ccg gag aga cag ccc agg ttc gtg gtt tac      151
Glu Leu Lys Met Glu Leu Pro Glu Arg Gln Pro Arg Phe Val Val Tyr
                25                30                35
agc tac aag tac gtg cgt gac gat ggc cga gtg tcc tac cct ttg tgt      199
Ser Tyr Lys Tyr Val Arg Asp Gly Arg Val Ser Tyr Pro Leu Cys
                40                45                50
ttc atc ttc tcc agc cct gtg ggc tgc aag ccg gaa caa cag atg atg      247
Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Pro Glu Gln Gln Met Met
                55                60                65                70
tat gca ggg agt aaa aac agg ctg gtg cag aca gca gag ctc aca aag      295
Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln Thr Ala Glu Leu Thr Lys
                75                80                85

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gtg ttc gaa atc cgc acc act gat gac ctc act gag gcc tgg ctc caa      343
Val Phe Glu Ile Arg Thr Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln
          90                      95                      100
gaa aag ttg tct ttc ttt cgt tgatctctgg gctggggact gaattcctga      394
Glu Lys Leu Ser Phe Phe Arg
          105
tgtctgagtc ctcaaggtga ctggggactt ggaacccta ggacctgaac aaccaagact      454
ttaaataaat tttaaaatgc aaaaaaaaaa aaaa      488

<210> 167
<211> 771
<212> DNA
<213> Homo sapiens
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<222> 48..356
<223> Von Heijne matrix
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      seq VYAFGLTAPSGS/KE
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<221> polyA_signal
<222> 742..747
<220>
<221> polyA_site
<222> 760..771
<400> 167
ccacagccct tttcaggacc caaacaaccg cagccgctgt tcccagg atg gtg atc      56
                                   Met Val Ile
cgt gta tat att gca tct tcc tct ggc tct aca gcg att aag aag aaa      104
Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile Lys Lys Lys
-100                      -95                      -90                      -85
caa caa gat gtg ctt ggt ttc cta gaa gcc aac aaa ata gga ttt gaa      152
Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile Gly Phe Glu
          -80                      -75                      -70
gaa aaa gat att gca gcc aat gaa gag aat cgg aag tgg atg aga gaa      200
Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp Met Arg Glu
          -65                      -60                      -55
aat gta cct gag aat agt cga cca gcc aca ggt aac ccc ctg cca cct      248
Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro Leu Pro Pro
          -50                      -45                      -40
cag att ttc aat gaa agc cag tat cgc ggg gac tat gat gcc ttc ttt      296
Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp Ala Phe Phe
          -35                      -30                      -25
gaa gcc aga gaa aat aat gca gtg tat gcc ttc tta ggc ttg aca gcc      344
Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly Leu Thr Ala
-20                      -15                      -10                      -5
cca tct ggt tca aag gaa gca gaa gtg caa gca aag cag caa gca      389
Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln Gln Ala
          1                      5                      10
tgaaccttga gcactgtgct ttaagcatcc tgaaaaatga gtctccattg cttttataaa      449
atagcagaat tagcttttgc tcaaaagaaa taggcttaat gttgaaataa tagattagtt      509
gggtttttcac atgcaaacac tcaaaatgaa tacaaaatta aaatttgaac attatggtga      569
ttatggtgag gagaatggga tattaacata aaattatatt aataagtaga tatcgtagaa      629
atagtgttgt tacctgccaa gccatcctgt atacaccaat gattttacaa agaaaacacc      689
cttccctcct tctgccatta ctatggcaac ctaagtgtat ctgcagctct acattaaaaa      749
ggagaaagag aaaaaaaaaa aa      771

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<210> 168

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<211> 959
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<222> 69..359
<223> Von Heijne matrix
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      seq RLPLVVSFIASSS/AN
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<221> polyA_signal
<222> 927..932
<220>
<221> polyA_site
<222> 947..959
<400> 168
cggagagaac caggcagccc agaaacccca ggcgtggaga ttgatacctgc gagagaaggg      60
ggttcatc atg gcg gat gac cta aag cga ttc ttg tat aaa aag tta cca      110
      Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro
            -95                    -90                    -85

agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga gat gga gta      158
Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val
            -80                    -75                    -70

cct gtt att aaa gtg gca aat gac aat gct cca gag cat gct ttg cga      206
Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg
            -65                    -60                    -55

cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa gga agc aaa      254
Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys
            -50                    -45                    -40

ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat aac acc tac      302
Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr
            -35                    -30                    -25                    -20

cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt ttc ata gcc      350
Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala
            -15                    -10                    -5

agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt      398
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu
            1                    5                    10

gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct      440
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
            15                    20                    25

taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc      500
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg cccctttttc      560
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt      620
ttctggtgta gggctctttct tatttagtga gatctagggg taccacagaa atggttcagt      680
ctatcacagc tcccatggag ttagtctggt caccagatat ggatgagaga ttctattcag      740
tggatcagaa tcaaactggt acattgatcc acttgagccg ttaagtgctg ccaattgtac      800
aatatgcccc ggcttgacaga ataaagccaa ctttttattg tgaataataa taaggacata      860
tttttcttca gattatgttt tatttctttg cattgagtga ggaacataaa atggcttggt      920
aaaagtaata aaatcagtac aatcactaaa aaaaaaaaaa      959

<210> 169
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<222> 33..98

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<222> 455..464
<400> 169
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                                Met Lys Pro Val Leu Pro Leu
                                -20
cag ttc ctg gtg gtg ttc tgc cta gca ctg cag ctg gtg cct ggg agt      101
Gln Phe Leu Val Val Phe Cys Leu Ala Leu Gln Leu Val Pro Gly Ser
-15          -10          -5          1
ccc aag cag cgt gtt ctg aag tat atc ttg gaa cct cca ccc tgc ata      149
Pro Lys Gln Arg Val Leu Lys Tyr Ile Leu Glu Pro Pro Pro Cys Ile
          5          10          15
tca gca cct gaa aac tgt act cac ctg tgt aca atg cag gaa gat tgc      197
Ser Ala Pro Glu Asn Cys Thr His Leu Cys Thr Met Gln Glu Asp Cys
          20          25          30
gag aaa gga ttt cag tgc tgt tcc tcc ttc tgt ggg ata gtc tgt tca      245
Glu Lys Gly Phe Gln Cys Cys Ser Ser Phe Cys Gly Ile Val Cys Ser
          35          40          45
tca gaa aca ttt caa aag cgc aac aga atc aaa cac aag ggc tca gaa      293
Ser Glu Thr Phe Gln Lys Arg Asn Arg Ile Lys His Lys Gly Ser Glu
          50          55          60          65
gtc atc atg cct gcc aac tgaggcatat ttcctagatc attttgcctc      341
Val Ile Met Pro Ala Asn
          70
tacgatgttt tttcttggtc cacctttagg aaggtattga gaagcaagaa actggaggcc      401
caatatctaa cctgcaaatc gtttttgagt ttggcaataa aggctaactt accaaaaaaa      461
aaa                                                                464

<210> 170
<211> 799
<212> DNA
<213> Homo sapiens
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<222> 110..235
<223> Von Heijne matrix
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      seq LLFDLVCHEFCQS/DD
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<221> polyA_site
<222> 787..799
<400> 170
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agctgccaaa caagtacggt ctgaaaatcc agaatggcct gatgtttac atg cac att      118
                                Met His Ile
                                -40
tta caa ctg ctt act aca gtg gat gat gga att caa gca att gta cat      166
Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His

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40 45 50  
 ggt gtc ttc aac ctg tgaaatggga tcataatcac tgccttacct ccctcacggt 254  
 Gly Val Phe Asn Leu  
 55  
 tgttgtgagg actgagtgtg tggaagtttt tcataaactt tggatgctag tgtaaaaaaa 314  
 aaaaaa 320  
  
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 <211> 331  
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 <213> Homo sapiens  
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 <222> 129..209  
 <223> Von Heijne matrix  
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 seq CLLSYIALGAIHA/KI  
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 <222> 318..331  
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 aaaaggaa atg aac agg gtc cct gct gat tct cca aat atg tgt cta atc 170  
 Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile  
 -25 -20 -15  
 tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca aaa atc tgt 218  
 Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys  
 -10 -5 1  
 agg aga gca ttc cag gaa gag gga aga gca aat gca aag acg ggc gtg 266  
 Arg Arg Ala Phe Gln Glu Gly Arg Ala Asn Ala Lys Thr Gly Val  
 5 10 15  
 aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc ttggaatagc 316  
 Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys  
 20 25  
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 seq IILTAVYFALSIS/LH  
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 <222> 1042..1047  
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 <222> 1063..1075  
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 gagaaaacag aaggaag atg ctc cag acc agt aac tac agc ctg gtg ctc 110  
 Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu  
 -90 -85

tct ctg cag ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc	158
Ser Leu Gln Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe	
-80 -75 -70	
tca gaa ctg ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc	206
Ser Glu Leu Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile	
-65 -60 -55	
atc cag gat att gca gtc ctc ttc aac atc atc atc att ttc ctc atg	254
Ile Gln Asp Ile Ala Val Leu Phe Asn Ile Ile Ile Phe Leu Met	
-50 -45 -40	
ttc ttc aac acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc	302
Phe Phe Asn Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe	
-35 -30 -25 -20	
cat aag ttc aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc	350
His Lys Phe Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu	
-15 -10 -5	
agc atc tcc ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc	398
Ser Ile Ser Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser	
1 5 10	
aac agc ttc ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag	446
Asn Ser Phe Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln	
15 20 25	
aga cta gca gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta	494
Arg Leu Ala Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val	
30 35 40 45	
aga cta ggc gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag	542
Arg Leu Gly Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys	
50 55 60	
gag ttc atg caa gtt cga agg tgacctctg tcacactgat ggatactttt	593
Glu Phe Met Gln Val Arg Arg	
65	
ccttcctgat agaagccaca tttgctgctt tgcagggaga gttggcccta tgcattggca	653
aacagctgga ctttccaagg aagggttcaga ctactgtgt tcagcattca agaaggaaga	713
ccccctct tgcacaatta gagtgcctcc atcggtctcc agtgccgcat cccttccttg	773
ccttctacct ctgttcacc cccttccttc ctctcctctc tgtaccattc attctccctg	833
accggccttt cttgccgagg gttctgtggc tcttaccctt gtgaagcttt tccttttagcc	893
tgggacagaa ggacctccc gcccccaaag gatctcccag tgaccaaagg atgcgaagag	953
tgatagttac gtgctcctga ctgatcacac cgcagacatt tagattttta tacccaaggc	1013
actttaaaaa aatgttttat aaatagagaa taaattgaat tcttgttcca aaaaaaaaaa	1073
aa	1075

<210> 174

<211> 632

<212> DNA

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 62..265

<223> Von Heijne matrix

score 4.59999990463257

seq LPFSLVSM LVTQG/LV

<220>

<221> polyA\_signal

<222> 602..607

<220>

<221> polyA\_site

<222> 621..632

<400> 174

cactgggtca aggagtaagc agaggataaa caactggaag gagagcaagc acaaagtcac	60
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c atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt 109
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
      -65              -60              -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg 157
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
      -50              -45              -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa 205
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
      -35              -30              -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt 253
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
      -20              -15              -10              -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga 301
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
      1              5              10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc 349
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
      15              20              25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt 397
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
      30              35              40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt cca cag cat aac agg 445
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
      45              50              55              60
cac tgc ctc ctt acc tgt gag gaa tgc aaa ata aag cat gga tta agt 493
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
      65              70              75
gag aag gga gac tct cag cct tca gct tcc taaattctgt gtctgtgact 543
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
      80              85
ttcgaagttt tttaaacctc tgaatttgta cacatttaaa atttcaagtg tacttttaaaa 603
taaaatactt ctaatgtataa aaaaaaaaaa 632

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<210> 175
<211> 430
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 402..407
<220>
<221> polyA_site
<222> 419..430
<400> 175

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gtattgggaa agtgatttgt gaa atg aaa gta gaa gaa gag cat acc aat gca 53
Met Lys Val Glu Glu Glu His Thr Asn Ala
      1              5              10
ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata 101
Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile
      15              20              25
tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt 149
Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser
      30              35              40
gtc gat atg aac ata acg tac atg tca cct gca aaa tta gga gag gat 197
Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp
      45              50              55
ata gtg att aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt 245
Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe

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60	65	70	
acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta ata gca caa			293
Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln			
75	80	85	90
gga aga cac aca aaa cac ctg gga aac tgagagaaca gcagaatgac			340
Gly Arg His Thr Lys His Leu Gly Asn			
95			
ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg			400
aaataaacta gcaaaaccaa aaaaaaaaaa			430

<210> 176  
 <211> 185  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> sig\_peptide  
 <222> 42..113  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq ILFNLLIFLCGFT/NY

<220>  
 <221> polyA\_site  
 <222> 172..185  
 <400> 176  
 ctttcagaac tcaactgccaa gagccctgaa caggagccac c atg cag tgc ttc agc 56  
 Met Gln Cys Phe Ser  
 -20  
 ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt 104  
 Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys  
 -15 -10 -5  
 ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg 152  
 Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met  
 1 5 10  
 cat aaa cct gtt aca atg taaaaaaaaa aaaaaa 185  
 His Lys Pro Val Thr Met  
 15

<210> 177  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> sig\_peptide  
 <222> 108..170  
 <223> Von Heijne matrix  
 score 5.5  
 seq SFLPSALVIWTS/AF

<220>  
 <221> polyA\_signal  
 <222> 550..555  
 <220>  
 <221> polyA\_site  
 <222> 574..585  
 <400> 177  
 cacgttcctg ttgagtacac gttcctgttg atttacaaaa ggtgcaggta tgagcaggtc 60  
 tgaagactaa cattttgtga agttgtataaa cagaaaaacct gttagaa atg tgg tgg 116  
 Met Trp Trp  
 -20

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ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca      164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
-15 -10 -5
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat      212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
1 5 10
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca      260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
15 20 25 30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt      308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys
35 40 45
caa aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa      364
Gln Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt      424
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact gataaatatg      484
gtaagggtggg cttttcccc tgtgtaattg gctactatgt cttactgagc caagttgtaa      544
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa a      585

<210> 178
<211> 613
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 118..171
<223> Von Heijne matrix
score 5.90000009536743
seq ALALLWSLPASDL/GR
<220>
<221> polyA_signal
<222> 583..588
<220>
<221> polyA_site
<222> 602..613
<400> 178
ggggtgggtg gactagaagc atttgggagt agtggccagg ggccctggac gctagccacg      60
gagctgccgc acagagcctg gtgtccacaa gcttccaggt tggggttgga gcctggg      117
atg agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct      165
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
-15 -10 -5
gac ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt      213
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
1 5 10
ctc atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc      261
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
15 20 25 30
aag agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt      309
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val
35 40 45
gta aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca      351
Val Thr Val Gly Gly Arg Val Gly Ser Thr Phe Val Ala
50 55 60
tgagtcgatg ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg      411
tcgaaaataa gcaccttggg aactaaaccc ctctaatagc tataaaggct ttagttctgt      471
attgattaag ttactgtaaa agcttgggtt tatttttgta ggacttaatg gctaagaatt      531
agaacatagc aagggggctc ctctgttgga gtaatgtaaa ttgtaattat aaataaacat      591
gcaaaccttt aaaaaaaaaa aa      613

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<210> 179
<211> 427
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 128..268
<223> Von Heijne matrix
      score 5.5
      seq SALLFFARPCVFC/FK
<220>
<221> polyA_signal
<222> 410..415
<220>
<221> polyA_site
<222> 424..427
<400> 179
agcttggtgatt tacactgggc aacgtgggtg gaatgtatct ggctcagaac tatgatatac      60
caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaag aagaaacccc      120
ctagtgc atg aga ctg cct cca gca ctg cct tca gga tat act gat tct      169
      Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser
              -45                      -40                      -35
act gct ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt      217
Thr Ala Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe
              -30                      -25                      -20
tcg tct cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt      265
Ser Ser Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe
              -15                      -10                      -5
tgc ttt aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca      313
Cys Phe Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr
      1              5              10              15
ttt cca aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg      361
Phe Pro Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly
      20              25              30
agg ttc taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa      417
Arg Phe
aaaaacaaaa      427

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<210> 180
<211> 905
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 149..457
<223> Von Heijne matrix
      score 4.90000009536743
      seq FLAQTTLRNVLG/TQ
<220>
<221> polyA_site
<222> 893..912
<400> 180
gctgcctggtt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc      60
tcaagaatga gatggattct aggggtgtctt cacctgagaa gcaagataaa gagaatttcg      120
tgggtgtcaa caataaacgg cttggtgt atg tgg ctg gat cct gtt ttc cct      172
      Met Trp Leu Asp Pro Val Phe Pro
              -100

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ctc ttt cct gtt ggt gat cat tac ctt ccc cat ctc cat atg gat gtg	220
Leu Phe Pro Val Gly Asp His Tyr Leu Pro His Leu His Met Asp Val	
-95 -90 -85 -80	
ctt gaa ggt ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aaa	268
Leu Glu Gly Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys	
-75 -70 -65	
gtt gac ctc cga aca gtt act tgc aac att cct cca caa gag atc ctc	316
Val Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu	
-60 -55 -50	
acc aga gac tcc gta act act cag gta gat gga gtt gtc tat tac aga	364
Thr Arg Asp Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg	
-45 -40 -35	
atc tat agt gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa	412
Ile Tyr Ser Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln	
-30 -25 -20	
gca aca ttt ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca	460
Ala Thr Phe Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr	
-15 -10 -5 1	
cag acc ttg tcc cag atc tta gct gga cga gaa gag atc gcc cat agc	508
Gln Thr Leu Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser	
5 10 15	
atc cag act tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg	556
Ile Gln Thr Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val	
20 25 30	
gcc cga gtg gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga	604
Ala Arg Val Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg	
35 40 45	
tcc atg gca gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc	652
Ser Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val	
50 55 60 65	
ctt gca gct gaa gga gaa atg aat gct tcc aaa tcc ctg aag tca gcc	700
Leu Ala Ala Glu Gly Glu Met Asn Ala Ser Lys Ser Leu Lys Ser Ala	
70 75 80	
tcc atg gtg ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg	748
Ser Met Val Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu	
85 90 95	
cag acc ttg agc acg gta gcc acc gag aag aat tct acg att gtg ttt	796
Gln Thr Leu Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe	
100 105 110	
cct ctg ccc atg aat ata cta gag ggc att ggt ggc gtc agc tat gat	844
Pro Leu Pro Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp	
115 120 125	
aac cac aag aag ctt cca aat aaa gcc tgaggtcctc ttgcggtagt	891
Asn His Lys Lys Leu Pro Asn Lys Ala	
130 135	
caaaaaaaaaa aaaa	905
 <210> 181	
<211> 307	
<212> PRT	
<213> Homo sapiens	
<220>	
<221> SIGNAL	
<222> -13..-1	
<400> 181	
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu	
-10 -5 1	
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro	

5	10	15													
Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	Gln	Ala	Glu
20					25					30					35
Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	Ala	His	Ile
				40					45					50	
Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	Val	Lys	Leu
			55					60					65		
Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser	Gly	Pro	Cys
		70					75					80			
Lys	Thr	Arg	Gly	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	Gly	Ile	Arg
	85					90					95				
Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr	Lys	Gly	Leu
100					105					110					115
Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	Leu	Ser	Ser
				120					125					130	
Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	Asp	Leu	Thr
			135					140					145		
Val	Thr	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	Ser	Ser	Lys
	150						155					160			
Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Leu	Val	Met	Glu	Gly	Thr	Asp	Asp
	165					170					175				
Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	Lys	Val	Leu
180					185					190					195
Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser	Pro	Ala	Glu
				200					205					210	
Asp	Phe	Val	Leu	Val	Ala	Glu	Thr	Thr	Met	Ala	Arg	Ile	Arg	Arg	Val
		215						220					225		
Tyr	Val	Ser	Gly	Leu	Met	Lys	Gly	Gly	Ala	Asp	Leu	Phe	Val	Glu	Asn
	230						235					240			
Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser	Gly	Gly	Tyr
	245					250					255				
Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe	Ser	Met	Leu
260					265					270					275
Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile	Phe	Lys	Val
				280					285					290	

Lys Lys Lys

<210> 182

<211> 59

<212> PRT

<213> Homo sapiens

<400> 182

Met	Met	Tyr	Val	Ser	Ile	Glu	Met	Ser	Gly	Pro	Thr	Ile	Ser	His	Leu
1				5					10					15	
Phe	Asp	Tyr	Val	Val	Cys	Tyr	Ile	Tyr	Gly	Leu	Lys	Ser	Phe	Ser	Leu
			20					25					30		
Lys	Gln	Leu	Lys	Lys	Lys	Ser	Trp	Ser	Lys	Tyr	Leu	Phe	Glu	Ser	Cys
	35						40					45			
Cys	Tyr	Arg	Ser	Leu	Tyr	Val	Cys	Val	Phe	Ile					
	50					55									

<210> 183

<211> 97

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 183

Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly  
          -25                  -20                  -15  
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val  
          -10                  -5                  1  
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu  
5                  10                  15                  20  
His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro  
                  25                  30                  35  
Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu  
                  40                  45                  50  
Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val  
          55                  60                  65  
Ala

<210> 184

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -32...-1

<400> 184

Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala  
          -30                  -25                  -20  
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro  
          -15                  -10                  -5  
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser  
1                  5                  10                  15  
Thr Phe Ala His  
                  20

<210> 185

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -97...-1

<400> 185

Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val  
          -95                  -90                  -85  
Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val  
          -80                  -75                  -70  
Val Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly  
-65                  -60                  -55                  -50  
Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly  
                  -45                  -40                  -35  
Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val  
                  -30                  -25                  -20  
Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser  
          -15                  -10                  -5  
Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro  
1                  5                  10                  15  
Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser  
                  20                  25

<210> 186

<211> 230  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -24...-1  
 <400> 186  
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu  
                   -20                  -15                  -10  
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr  
                   -5                  1                  5  
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys  
       10                  15                  20  
 Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys  
 25                  30                  35                  40  
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala  
                   45                  50                  55  
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile  
                   60                  65                  70  
 Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg  
                   75                  80                  85  
 Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly  
       90                  95                  100  
 Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu  
 105                  110                  115                  120  
 Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile  
                   125                  130                  135  
 Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile  
                   140                  145                  150  
 Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser  
                   155                  160                  165  
 Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser  
       170                  175                  180  
 Pro Arg Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr  
 185                  190                  195                  200  
 Ser Leu Thr Gly Tyr Val  
                   205

<210> 187  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -32...-1  
 <400> 187  
 Met Phe Ala Leu Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
                   -30                  -25                  -20  
 Gly Tyr Gly Val Pro Met Leu Leu Ile Ala Gly Gly Ser Phe Gly  
                   -15                  -10                  -5  
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met  
 1                  5                  10                  15  
 Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu  
                   20                  25                  30  
 Ser Glu Tyr Glu Gly Ser Ile Cys  
                   35                  40

<210> 188

<211> 88  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -33..-1  
 <400> 188  
 Met Ser Gln Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly  
                   -30                  -25                  -20  
 Pro Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr  
                   -15                  -10                  -5  
 Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly  
   1                                  5                                  10                                  15  
 Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe  
                                   20                                  25                                  30  
 Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met  
                                   35                                  40                                  45  
 Asp Pro Lys Arg Lys Thr Lys Cys  
                   50                                  55

<210> 189  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -32..-1  
 <400> 189  
 Met Phe Ala Pro Ala Val Thr Arg Ala Phe Arg Lys Asn Lys Thr Leu  
                   -30                  -25                  -20  
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly  
                   -15                  -10                  -5  
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met  
   1                                  5                                  10                                  15  
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu  
                                   20                                  25                                  30  
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn  
                                   35                                  40                                  45  
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg  
                   50                                  55                                  60  
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr  
   65                                  70

<210> 190  
 <211> 267  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -21..-1  
 <400> 190  
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val  
                   -20                  -15                  -10  
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr  
   -5                                  1                                  5                                  10  
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr  
                                   15                                  20                                  25  
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala



30	35	40
Val Leu Cys Ile Ala Thr	Ile Tyr Val Arg Tyr Lys	Gln Val His Ala
45	50	55
Leu Ser Pro Glu Glu Asn	Val Ile Ile Lys Leu Asn	Lys Ala Gly Leu
60	65	70
Val Leu Gly Ile Leu Ser	Cys Leu Gly Leu Ser	Ile Val Ala Asn Phe
	80	85
Gln Lys Thr Thr Leu Phe	Ala Ala His Val Ser	Gly Ala Val Leu Thr
	95	100
Phe Gly Met Gly Ser Leu	Tyr Met Phe Val Gln	Thr Ile Leu Ser Tyr
	110	115
Gln Met Gln Pro Lys Ile	His Gly Lys Gln Val	Phe Trp Ile Arg Leu
	125	130
Leu Leu Val Ile Trp Cys	Gly Val Ser Ala Leu	Ser Met Leu Thr Cys
140	145	150
Ser Ser Val Leu His Ser	Gly Asn Phe Gly Thr	Asp Leu Glu Gln Lys
	160	165
Leu His Trp Asn Pro Glu	Asp Lys Gly Tyr Ala	Leu His Met Ile Thr
	175	180
Thr Ala Ala Glu Trp Ser	Met Ser Phe Ser Phe	Phe Gly Phe Phe Leu
	190	195
Thr Tyr Ile Arg Asp Phe	Gln Lys Ile Ser Leu	Arg Val Glu Ala Asn
	205	210
Leu His Gly Leu Thr Leu	Tyr Asp Thr Ala Pro	Cys Pro Ile Asn Asn
220	225	230
Glu Arg Thr Arg Leu Leu	Ser Arg Asp Ile Arg	
	240	245

<210> 191

<211> 108

<212> PRT

<213> Homo sapiens

<400> 191

Met Gly Cys Val Phe Gln	Ser Thr Glu Asp Lys Cys	Ile Phe Lys Ile
1	5	10
Asp Trp Thr Leu Ser Pro	Gly Glu His Ala Lys	Asp Glu Tyr Val Leu
	20	25
Tyr Tyr Tyr Ser Asn Leu	Ser Val Pro Ile Gly	Arg Phe Gln Asn Arg
	35	40
Val His Leu Met Gly Asp	Ile Leu Cys Asn Asp	Gly Ser Leu Leu Leu
	50	55
Gln Asp Val Gln Glu Ala	Asp Gln Gly Thr Tyr	Ile Cys Glu Ile Arg
65	70	75
Leu Lys Gly Glu Ser Gln	Val Phe Lys Lys Ala	Val Val Leu His Val
	85	90
Leu Pro Glu Glu Pro Lys	Gly Thr Gln Met Leu	Thr
	100	105

<210> 192

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -46...-1

<400> 192

Met Ser Val Phe Trp Gly	Phe Val Gly Phe Leu	Val Pro Trp Phe Ile
-45	-40	-35

Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys  
 -30 -25 -20 -15  
 Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu  
 -10 -5 1  
 Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu  
 5 10 15  
 Lys Tyr His Trp Pro  
 20

<210> 193  
 <211> 251  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -28..-1  
 <400> 193

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro  
 -25 -20 -15  
 Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr  
 -10 -5 1  
 Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro  
 5 10 15 20  
 Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg  
 25 30 35  
 Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr  
 40 45 50  
 Glu Phe Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr  
 55 60 65  
 Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser  
 70 75 80  
 Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe  
 85 90 95 100  
 Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys  
 105 110 115  
 Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Leu Val  
 120 125 130  
 Val Glu Met Gly Gly Arg Cys Glu Phe Glu Glu Val Gln Gly Phe Leu  
 135 140 145  
 Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg  
 150 155 160  
 Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn  
 165 170 175 180  
 Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala Asn Met Leu  
 185 190 195  
 Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His Lys Gly Lys  
 200 205 210  
 Tyr Trp Gly Lys Phe Tyr Met Pro Lys Arg Val  
 215 220

<210> 194  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -48..-1  
 <400> 194

Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser  
                   -45                  -40                  -35  
 Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu  
                   -30                  -25                  -20  
 Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro  
                   -15                  -10                  -5  
 Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr  
 1                  5                  10                  15  
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu  
                   20                  25                  30  
 Phe Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys  
                   35                  40                  45  
 Glu Val Leu  
                   50

<210> 195  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -31...-1  
 <400> 195

Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro  
                   -30                  -25                  -20  
 Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro  
                   -15                  -10                  -5                  1  
 Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser  
                   5                  10                  15  
 Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser  
                   20                  25                  30  
 Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp  
                   35                  40                  45  
 Leu  
 50

<210> 196  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens  
 <400> 196

Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr  
 1                  5                  10                  15  
 Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly  
                   20                  25                  30  
 Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro  
                   35                  40                  45  
 Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr Tyr Ile  
                   50                  55                  60  
 Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe  
 65                  70                  75                  80  
 Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val  
                   85                  90                  95  
 Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu  
                   100                  105                  110  
 Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser His Asn His  
                   115                  120                  125  
 Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr Val Thr Ser

130                      135                      140  
 Val Ser Thr Lys Lys Lys  
 145                      150  
  
 <210> 197  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -45...-1  
 <400> 197  
 Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
 -45                      -40                      -35                      -30  
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
                          -25                      -20                      -15  
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His  
                          -10                      -5                      1  
 Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys  
   5                      10                      15  
 Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
 20                      25                      30                      35  
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
                          40                      45                      50  
 Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn  
                          55                      60                      65  
 Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp  
                          70                      75                      80  
 Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala  
   85                      90                      95  
 Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro  
 100                      105                      110                      115  
 Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe  
                          120                      125                      130  
 Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala  
                          135                      140                      145  
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu  
                          150                      155                      160  
 Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala  
   165                      170                      175  
 Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys Gln  
 180                      185                      190                      195  
 Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His  
                          200                      205                      210  
 Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile  
                          215                      220                      225  
 Leu

<210> 198  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -37...-1  
 <400> 198  
 Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro  
                          -35                      -30                      -25

Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His
-20						-15					-10				
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr
-5					1			5						10	
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser
		15						20					25		
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Leu	Ala	Asn	Ile	Val	Glu	Arg
	30					35						40			
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu
	45					50					55				
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg
60					65					70					75
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His
				80					85					90	
His	Thr	Val	Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu
			95					100					105		
Gln	Ala	Val	Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys
	110						115						120		
Leu	Glu	Ala	Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val
	125					130					135				
Gln	Thr	Glu	Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser
140					145					150					155
Ile	Leu	Asn	Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu
				160					165					170	
Glu	Lys	Lys	Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val
			175				180						185		
Gln	Gln	Lys	Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg
	190						195					200			
Ser	Gln	Trp	Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met
	205					210					215				
Lys	Trp	Ser	Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys
220					225					230					235
Lys	Leu	Lys	Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln
				240					245					250	
Met	Phe	Arg	Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr
			255					260					265		
Leu	Asn	Ser	Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln
	270					275						280			
Arg	Gln	Val	Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr
	285					290					295				
Gly	Val	Leu	Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu
300					305					310					315
Val	Asp	Val	Ser	Lys	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg
				320					325					330	
Thr	Tyr	Ser	Arg	His	Met	Lys	Tyr	Val	Val	Arg	Arg	Cys	Ala	Asn	Arg
			335					340					345		
Gln	Asn	Leu	Tyr	Thr	Lys	Tyr	Arg	Pro	Leu	Phe	Gly	Tyr	Trp	Val	Ile
	350					355						360			
Gly	Leu	Gln	Asn	Lys	Cys	Lys	Tyr	Gly	Ala	Lys	Lys	Lys			
	365					370					375				

<210> 199  
 <211> 393  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 199

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
                  -15                  -10                  -5  
Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys  
                  1                  5                  10  
Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg  
                  15                  20                  25  
Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His  
                  30                  35                  40                  45  
Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp  
                  50                  55                  60  
Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr  
                  65                  70                  75  
Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln  
                  80                  85                  90  
Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp  
                  95                  100                  105  
Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu  
                  110                  115                  120                  125  
His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe  
                  130                  135                  140  
Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr  
                  145                  150                  155  
Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu  
                  160                  165                  170  
Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met  
                  175                  180                  185  
Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu  
                  190                  195                  200                  205  
Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met  
                  210                  215                  220  
Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe  
                  225                  230                  235  
Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn  
                  240                  245                  250  
Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys  
                  255                  260                  265  
Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met  
                  270                  275                  280                  285  
Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg  
                  290                  295                  300  
Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser  
                  305                  310                  315  
Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg  
                  320                  325                  330  
His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu  
                  335                  340                  345  
Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln  
                  350                  355                  360                  365  
Gly Leu Asp Tyr Phe Tyr Asp Leu Leu  
                  370

<210> 200

<211> 381

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 200

Met	Leu	Leu	Ser	Ile	Gly	Met	Leu	Met	Leu	Ser	Ala	Thr	Gln	Val	Tyr
			-10				-5						1		
Thr	Val	Leu	Thr	Val	Gln	Leu	Phe	Ala	Phe	Leu	Asn	Pro	Leu	Pro	Val
5					10					15					
Glu	Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	Glu	Asn	Ala	Ser	Gln	Thr	Phe
20					25				30						35
Asp	Asp	Leu	Pro	Ala	Arg	Phe	Gly	Tyr	Arg	Leu	Pro	Ala	Glu	Gly	Leu
				40					45					50	
Lys	Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	Glu	Asn	Ala	Cys	Glu	Pro	Ile
			55				60					65			
Val	Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Val	Leu
			70				75					80			
Ile	Arg	Arg	Leu	Asp	Cys	Asn	Phe	Asp	Ile	Lys	Val	Leu	Asn	Ala	Gln
85					90					95					
Arg	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	His	Asn	Val	Asp	Ser	Asp	Asp
100					105					110					115
Leu	Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile	Glu	Val	Leu	Lys	Lys	Ile	Asp
				120					125					130	
Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asp
			135				140						145		
Glu	Phe	Thr	Tyr	Glu	Lys	Gly	Gly	His	Leu	Ile	Leu	Val	Pro	Glu	Phe
		150				155						160			
Ser	Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	Pro	Phe	Leu	Ile	Ile	Val	Gly
165					170					175					
Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Phe	Val	Gln
180					185					190					195
Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys
				200					205					210	
Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys
			215					220					225		
Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu
		230					235					240			
Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr
	245					250					255				
Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser
260					265					270					275
Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu
				280					285					290	
Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Ser	Val	Ser	Ala
			295					300					305		
Gln	Ser	Phe	Gly	Ala	Leu	Ser	Glu	Ser	Arg	Ser	His	Gln	Asn	Met	Thr
		310					315					320			
Glu	Ser	Ser	Asp	Tyr	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr	Asp	Ser	Ser
		325				330					335				
Asp	Ala	Glu	Asn	Glu	Ile	Asn	Glu	His	Asp	Val	Val	Val	Gln	Leu	Gln
340					345					350					355
Pro	Asn	Gly	Glu	Arg	Asp	Tyr	Asn	Ile	Ala	Asn	Thr	Val			
				360					365						

<210> 201

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 201

Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe  
-40 -35 -30  
Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe  
-25 -20 -15  
Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp  
-10 -5 1 5  
Met Cys Leu Lys Ile Ile Arg Glu Tyr Glu Arg Ala Val Val Phe Arg  
10 15 20  
Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu  
25 30 35  
Val Leu Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val  
40 45 50  
Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr  
55 60 65 70  
Thr Gln Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser  
75 80 85  
Ala Val Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala  
90 95 100  
Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile  
105 110 115  
Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp  
120 125 130  
Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys  
135 140 145 150  
Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala  
155 160 165  
Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu  
170 175 180  
Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu  
185 190 195  
Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val  
200 205 210  
Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile  
215 220 225 230  
Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro  
235 240 245  
Asn Lys Ala

<210> 202

<211> 92

<212> PRT

<213> Homo sapiens

<400> 202

Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly  
1 5 10 15  
Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr  
20 25 30  
Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu  
35 40 45  
Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys  
50 55 60  
Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe  
65 70 75 80  
Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser  
85 90

<210> 203



<211> 127  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -63..-1  
 <400> 203  
 Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu  
                   -60                  -55                  -50  
 Pro Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr  
                   -45                  -40                  -35  
 Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met  
                   -30                  -25                  -20  
 Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala  
                   -15                  -10                  -5                  1  
 Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe  
                   5                  10                  15  
 Ile Trp Ser Arg Tyr Ser Leu Val Ile Ile Pro Lys Asn Trp Ser Leu  
                   20                  25                  30  
 Phe Ala Val Asn Phe Phe Val Gly Ala Ala Gly Ala Ser Gln Leu Phe  
                   35                  40                  45  
 Arg Ile Trp Arg Tyr Asn Gln Glu Leu Lys Ala Lys Ala His Lys  
 50                  55                  60

<210> 204  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -20..-1  
 <400> 204  
 Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly  
                   -20                  -15                  -10                  -5  
 Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg  
                   1                  5                  10  
 Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys  
                   15                  20                  25  
 Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln  
                   30                  35                  40  
 Ser Val Val Glu Val Thr Val Thr Val Pro Pro Asn Lys Val Ala His  
 45                  50                  55                  60  
 Ser Gly Phe Gly

<210> 205  
 <211> 182  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -20..-1  
 <400> 205  
 Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly  
                   -20                  -15                  -10                  -5  
 Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg  
                   1                  5                  10  
 Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys  
                   15                  20                  25

Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln  
 30 35 40  
 Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu  
 45 50 55 60  
 Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile  
 65 70 75  
 Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn  
 80 85 90  
 Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp  
 95 100 105  
 Ile Ser Gly Thr Leu Lys Phe Ala Cys Gly Ser Ile Val Glu Glu Tyr  
 110 115 120  
 Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys  
 125 130 135 140  
 Asp Lys Leu Cys Ser Lys Arg Thr Asp Leu Cys Asp His Ala Leu His  
 145 150 155  
 Ile Ser His Asp Glu Leu  
 160

<210> 206  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -25..-1  
 <400> 206

Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala  
 -25 -20 -15 -10  
 Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr  
 -5 1 5  
 Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu  
 10 15 20  
 Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val  
 25 30 35  
 Ser Gln Gln Glu Glu Leu Lys  
 40 45

<210> 207  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens  
 <400> 207

Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe Leu  
 1 5 10 15  
 Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu Phe  
 20 25 30  
 Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu Gly  
 35 40 45  
 Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln Arg  
 50 55 60  
 Glu Ser Leu Thr Gly Pro Pro Tyr Leu  
 65 70

<210> 208  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -150..-1  
 <220>  
 <221> UNSURE  
 <222> -67  
 <223> Xaa = any one of the twenty amino acids  
 <400> 208  
 Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys Asp  
 -150 -145 -140 -135  
 Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala  
 -130 -125 -120  
 Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu Leu  
 -115 -110 -105  
 Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg Gly  
 -100 -95 -90  
 Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly Trp  
 -85 -80 -75  
 Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro Glu  
 -70 -65 -60 -55  
 Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg  
 -50 -45 -40  
 Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu Thr  
 -35 -30 -25  
 Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys  
 -20 -15 -10  
 Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser  
 -5 1 5 10  
 His Arg Ala Arg Gln Arg Lys Thr Ala  
 15

<210> 209  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -22..-1  
 <400> 209  
 Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala  
 -20 -15 -10  
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile  
 -5 1 5 10  
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala  
 15 20 25  
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly  
 30 35 40  
 Arg Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe  
 45 50

<210> 210  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -54..-1  
 <400> 210

Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp  
                   -50                  -45                  -40  
 Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala  
                   -35                  -30                  -25  
 Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu  
                   -20                  -15                  -10  
 Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile  
                   -5                  1                  5                  10  
 Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys  
                   15                  20                  25  
 Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln  
                   30                  35                  40

<210> 211  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -22...-1  
 <400> 211

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala  
                   -20                  -15                  -10  
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile  
                   -5                  1                  5                  10  
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala  
                   15                  20                  25  
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe  
                   30                  35                  40  
 Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Glu  
                   45                  50                  55  
 Gly Ile Asn Val Phe Leu Lys Ser Lys Lys Lys Lys  
                   60                  65                  70

<210> 212  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -16...-1  
 <400> 212

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr  
                   -15                  -10                  -5  
 Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala  
                   1                  5                  10                  15  
 Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe  
                   20                  25                  30  
 Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile  
                   35                  40                  45  
 Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala  
                   50                  55                  60  
 Glu Ala Gly Ala Ser Leu Tyr Ser Pro  
                   65                  70

<210> 213  
 <211> 109  
 <212> PRT

<213> Homo sapiens

<400> 213

```
Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu Phe
1          5          10          15
Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg Gln
20        25        30
Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg
35        40        45
Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys Lys
50        55        60
Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln
65        70        75        80
Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr Thr Asp Asp Leu
85        90        95
Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe Arg
100       105
```

<210> 214

<211> 114

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -103...-1

<400> 214

```
Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
          -100          -95          -90
Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
          -85          -80          -75
Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
          -70          -65          -60
Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro
          -55          -50          -45          -40
Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp
          -35          -30          -25
Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly
          -20          -15          -10
Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln
          -5          1          5
Gln Ala
10
```

<210> 215

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -97...-1

<400> 215

```
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
          -95          -90          -85
Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
          -80          -75          -70
Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
          -65          -60          -55          -50
Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
          -45          -40          -35
```

Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val  
                   -30                  -25                  -20  
 Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser  
                   -15                  -10                  -5  
 Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro  
       1                  5                  10                  15  
 Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser  
                   20                  25

<210> 216  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -22..-1  
 <400> 216

Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys Leu Ala  
                   -20                  -15                  -10  
 Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys Tyr Ile  
       -5                  1                  5                  10  
 Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr His Leu  
                   15                  20                  25  
 Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys Ser Ser  
                   30                  35                  40  
 Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg Asn Arg  
       45                  50                  55  
 Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn  
       60                  65                  70

<210> 217  
 <211> 207  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -42..-1  
 <400> 217

Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala  
                   -40                  -35                  -30  
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe  
       -25                  -20                  -15  
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile  
       -10                  -5                  1                  5  
 Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser  
                   10                  15                  20  
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys  
       25                  30                  35  
 Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met  
       40                  45                  50  
 Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu  
       55                  60                  65                  70  
 Glu Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile  
                   75                  80                  85  
 Leu Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu  
                   90                  95                  100  
 Thr Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys  
           105                  110                  115

Gln Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro  
 120 125 130  
 Val Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu  
 135 140 145 150  
 Ala Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr  
 155 160 165

<210> 218  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens  
 <400> 218

Met Pro His Ser Lys Pro Leu Asp Trp Gly Leu Ser Ser Val Ala Glu  
 1 5 10 15  
 Cys Pro Ala Glu Leu Phe Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly  
 20 25 30  
 Pro Gly Leu Asp Ile Leu Arg Cys Val Leu Ser Pro Trp Ala Ser His  
 35 40 45  
 Phe Pro Ser Leu Ser Leu Gly Val Phe Asn Leu  
 50 55

<210> 219  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -27..-1  
 <400> 219

Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu  
 -25 -20 -15  
 Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg  
 -10 -5 1 5  
 Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala  
 10 15 20  
 Trp Cys Ile Gln Pro Trp Ala Lys  
 25

<210> 220  
 <211> 162  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -94..-1  
 <400> 220

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu  
 -90 -85 -80  
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln  
 -75 -70 -65  
 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala  
 -60 -55 -50  
 Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe  
 -45 -40 -35  
 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly  
 -30 -25 -20 -15  
 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His  
 -10 -5 1

Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp  
5 10 15  
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val  
20 25 30  
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro  
35 40 45 50  
His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val  
55 60 65  
Arg Arg

<210> 221  
<211> 154  
<212> PRT  
<213> Homo sapiens  
<220>  
<221> SIGNAL  
<222> -68..-1  
<400> 221

Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe  
-65 -60 -55  
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu  
-50 -45 -40  
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu  
-35 -30 -25  
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu  
-20 -15 -10 -5  
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg  
1 5 10  
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly  
15 20 25  
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe  
30 35 40  
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg  
45 50 55 60  
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser  
65 70 75  
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser  
80 85

<210> 222  
<211> 99  
<212> PRT  
<213> Homo sapiens  
<400> 222

Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr Leu His Gly  
1 5 10 15  
Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met Ala Leu Leu  
20 25 30  
Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met Asn Ile Thr  
35 40 45  
Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile Thr Ala His  
50 55 60  
Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val Gly Leu Thr  
65 70 75 80  
Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His Thr Lys His  
85 90 95  
Leu Gly Asn



<210> 223  
 <211> 43  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -24...-1  
 <400> 223  
 Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
                   -20                  -15                  -10  
 Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser  
                   -5                  1                  5  
 Pro Tyr Phe Lys Met His Lys Pro Val Thr Met  
           10                  15

<210> 224  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -21...-1  
 <400> 224  
 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val  
           -20                  -15                  -10  
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr  
   -5                  1                  5                  10  
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr  
                   15                  20                  25  
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala  
           30                  35                  40  
 Val Leu Cys Gln Lys  
           45

<210> 225  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -18...-1  
 <400> 225  
 Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser  
                   -15                  -10                  -5  
 Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val  
           1                  5                  10  
 Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr  
   15                  20                  25                  30  
 Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val  
                   35                  40                  45  
 Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala  
           50                  55                  60

<210> 226  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens  
 <220>

<221> SIGNAL

<222> -47...-1

<400> 226

Met	Arg	Leu	Pro	Pro	Ala	Leu	Pro	Ser	Gly	Tyr	Thr	Asp	Ser	Thr	Ala
		-45				-40						-35			
Leu	Glu	Gly	Leu	Val	Tyr	Tyr	Leu	Asn	Gln	Lys	Leu	Leu	Phe	Ser	Ser
	-30				-25					-20					
Pro	Ala	Ser	Ala	Leu	Leu	Phe	Phe	Ala	Arg	Pro	Cys	Val	Phe	Cys	Phe
-15				-10					-5						1
Lys	Ala	Ser	Lys	Met	Gly	Pro	Gln	Phe	Glu	Asn	Tyr	Pro	Thr	Phe	Pro
			5				10						15		
Thr	Tyr	Ser	Pro	Leu	Pro	Ile	Ile	Pro	Phe	Gln	Leu	His	Gly	Arg	Phe
		20				25						30			

<210> 227

<211> 241

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -103...-1

<400> 227

Met	Trp	Leu	Asp	Pro	Val	Phe	Pro	Leu	Phe	Pro	Val	Gly	Asp	His	Tyr
		-100				-95		-95				-90			
Leu	Pro	His	Leu	His	Met	Asp	Val	Leu	Glu	Gly	Leu	Ile	Leu	Val	Leu
	-85				-80						-75				
Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val	Thr	Cys
-70				-65						-60					
Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr	Thr	Gln
-55				-50					-45						-40
Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser	Ala	Val
			-35					-30						-25	
Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala	Gln	Thr
	-20						-15						-10		
Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile	Leu	Ala
	-5				1					5					
Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp	Asp	Ala
10				15					20					25	
Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys	Asp	Val
			30					35					40		
Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	Ala	Glu	Ala	Glu	Ala
	45						50					55			
Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	Glu	Gly	Glu	Met	Asn
	60					65					70				
Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu	Ser	Pro
	75				80						85				
Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	Ser	Thr	Val	Ala	Thr
90				95						100					105
Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	Met	Asn	Ile	Leu	Glu
			110					115					120		
Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	Lys	Leu	Pro	Asn	Lys
			125				130						135		

Ala